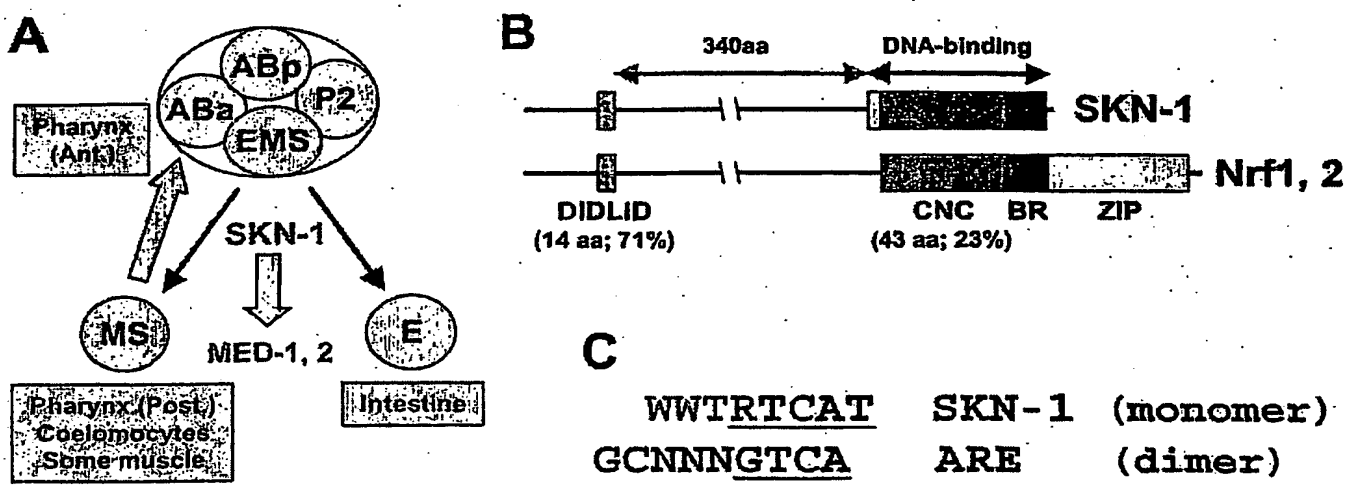

A
ABp
ABa
P2
EMS
Pharynx (Ant.)
SKN-1
MS
MED-1, 2
E
Pharynx (Post.)
Coelomocytes
Some muscle
Intestine
B
340aa
DNA-binding
SKN-1
Nrf1, 2
DIDLID
(14 aa; 71%)
CNC
BR
ZIP
(43 aa; 23%)
C
WWTRTCAT SKN-1 (monomer)
GCNNNGTCA ARE (dimer)

Fig. 1A-1C

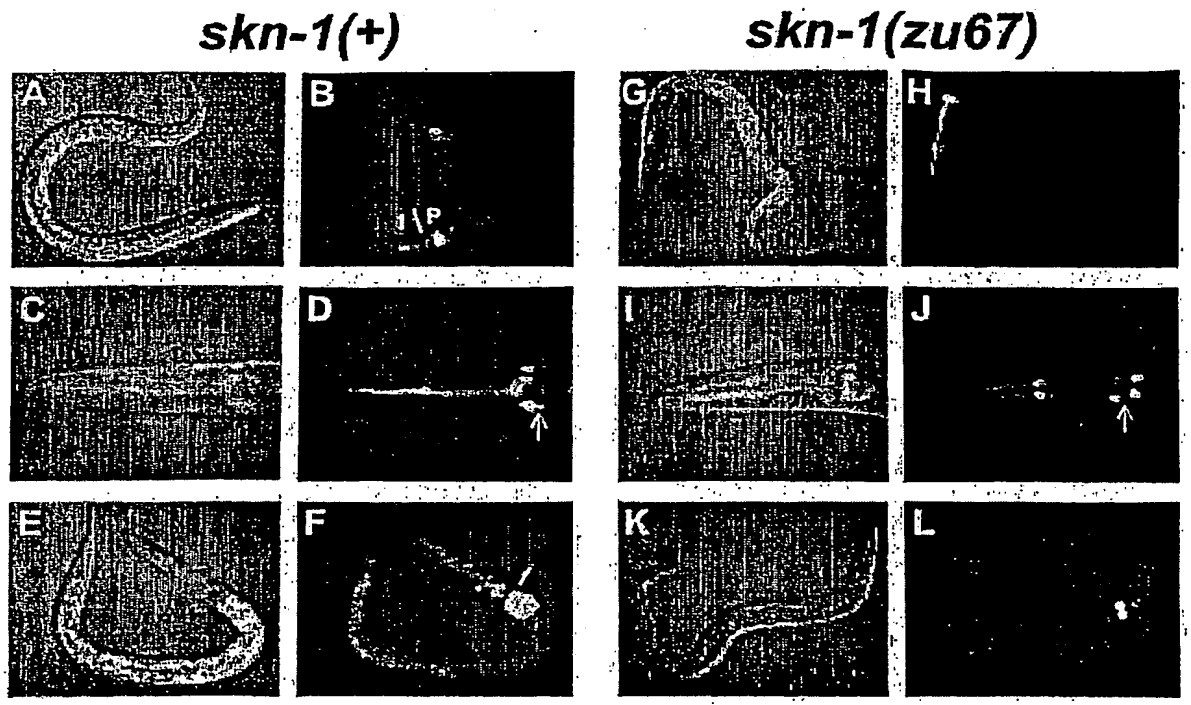
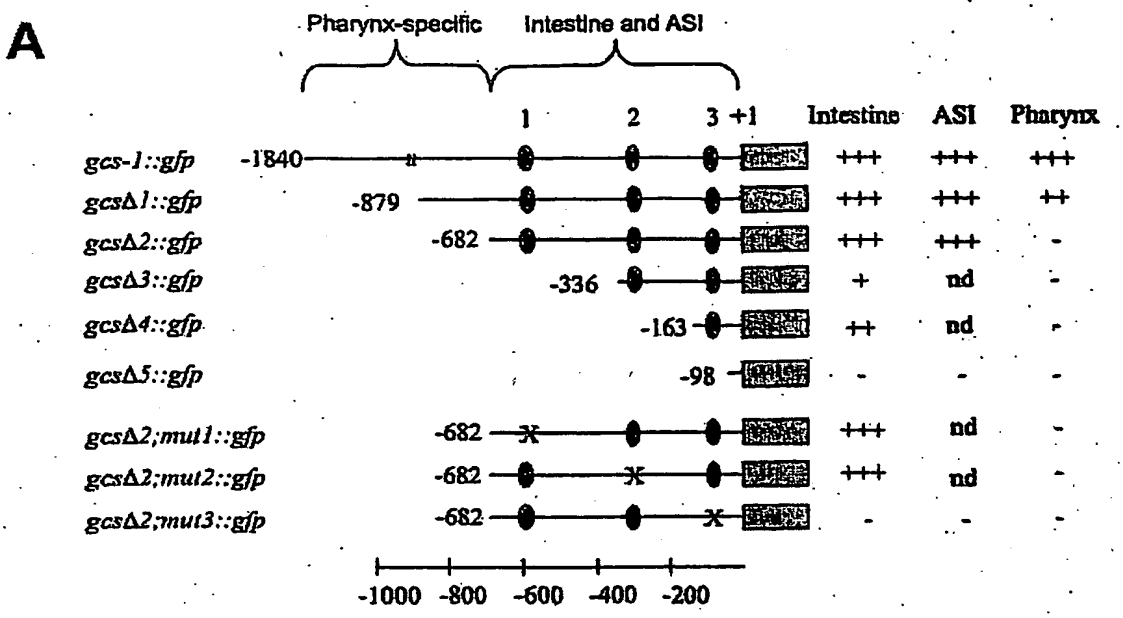
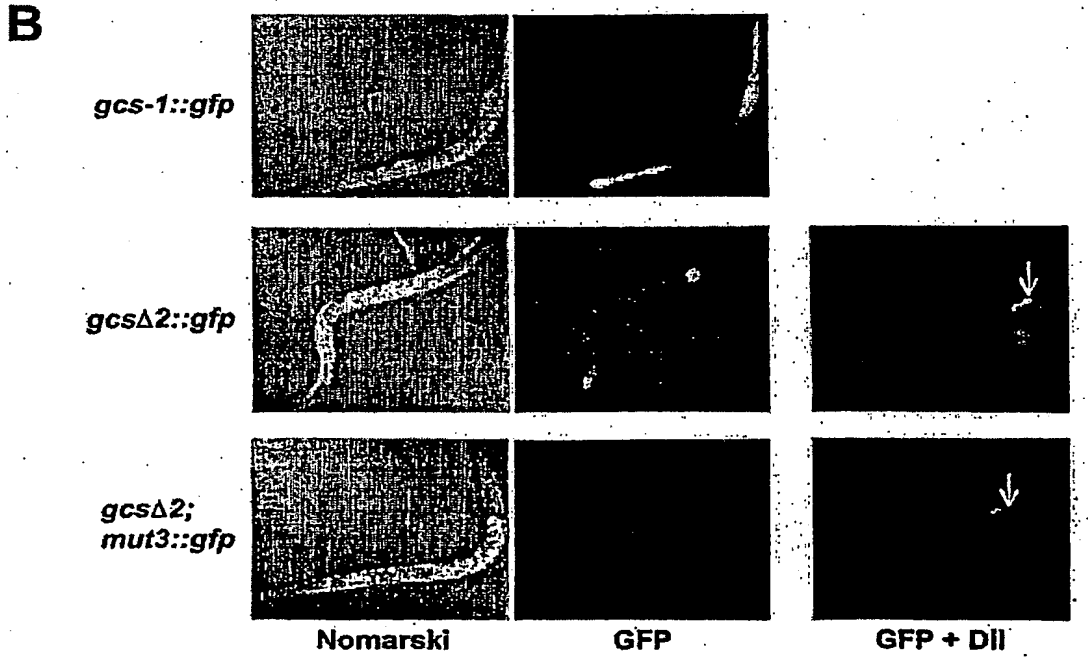


Fig. 2A-2L





C

```
gcs-1   -124  CA-CTTTATCATCATGA-GATTTAATGTTTCCTTTTGAT--TTTCT-83
med-1   -127  CACCTCTGTCATCATGATGATTTTTGGAG-CATTATCATCATTTCT-83
med-2   -127  CACCTCTGTCATCATGATGATTTTTAGAG-CATTATCATCATTTCT-83
```

Fig. 3A-3C

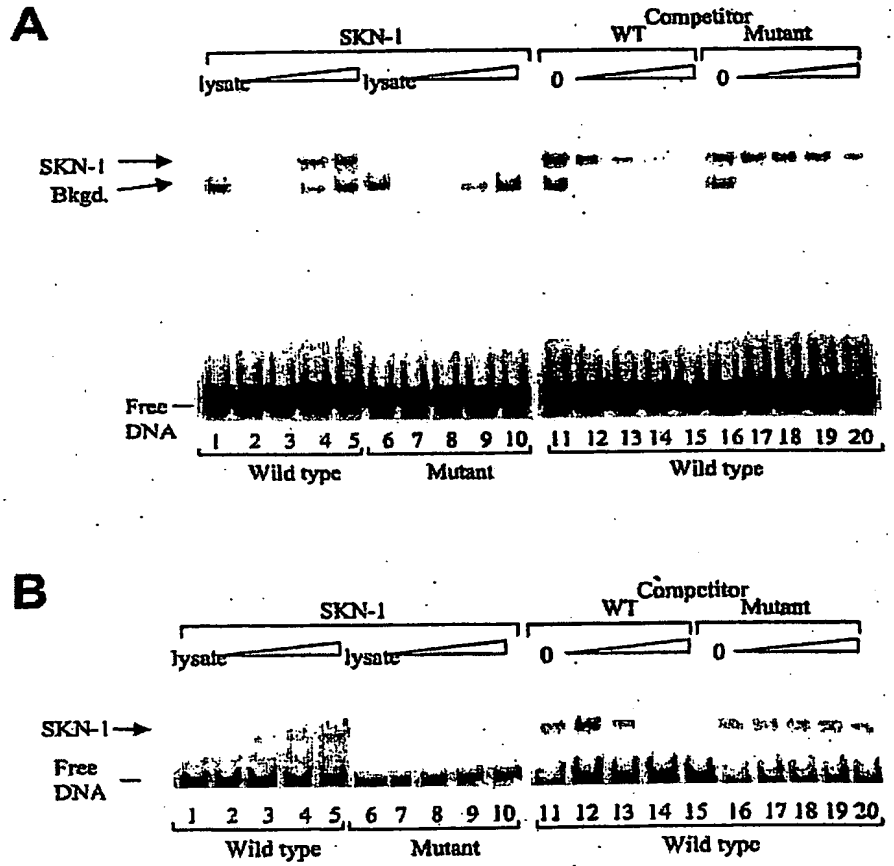


Fig. 4A-4B

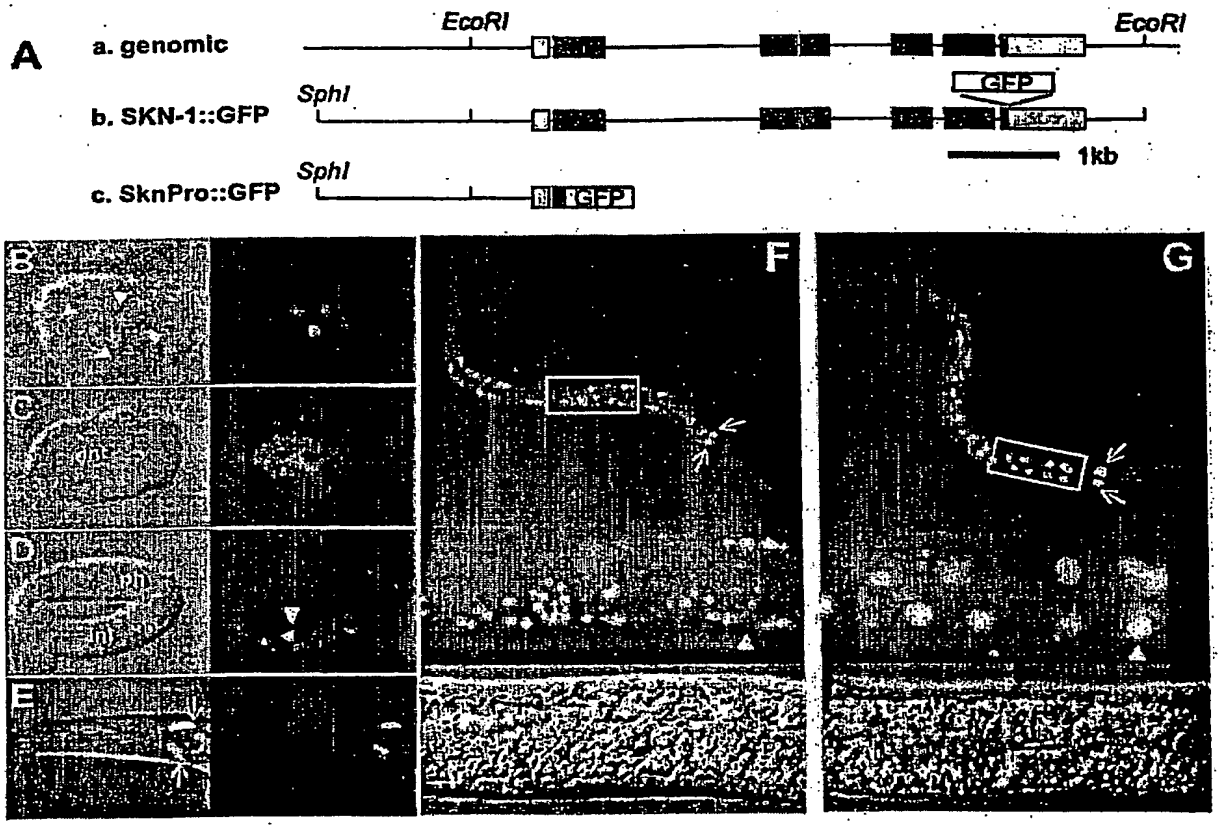


Fig. 5A-5G

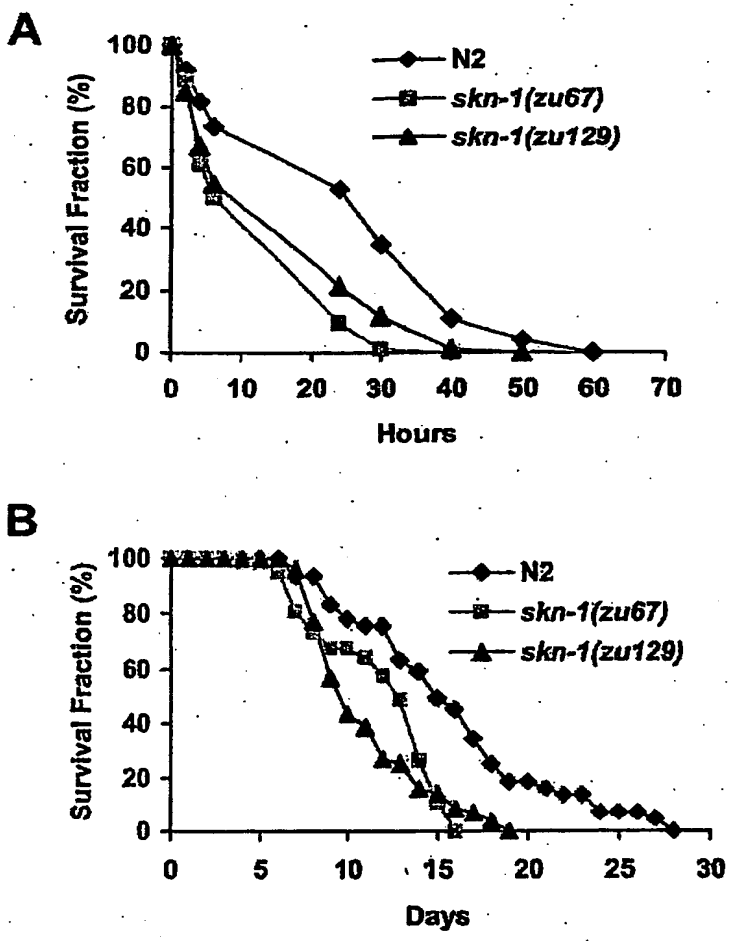
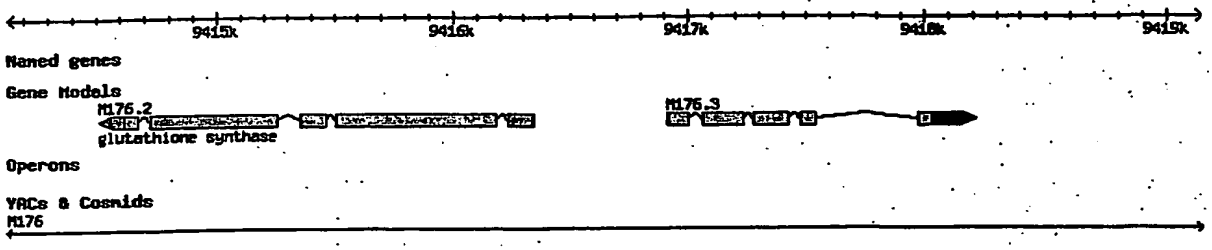


Fig. 6A-6B



The M176.2 gene is located on chromosome II. Regulatory sequences can be found e.g., in the region between 9416340 and 9415915. An exemplary sequence of this region is as follows:

GACAATTATCGATTAATAAAAGTTTAAACAGACACGAGAAATTAAATATAAAAAATTGAATTGTTTATTT

GTTGTTTTGTGTGTAGAAAAATAATTTTGATAGAAACAAAAAATTAGCGTAAAATAAATAGCTAGCGCAA

TACTCGTGCACGAGATGTGCGCCAGCAGCTCCTTGACGCAAAACGTGACGTTTAGCACCAAAATGATTTT
-378

TGCTCTTTGAGTTCTTTGTTTTCGGGAGCAAATTTCATGCCAATCCCTTTCTTTTTTTCAAATTTTCCTG

TTAAATTCATGTAATAACTATTATTCATGTCAATTACAACAAATAAGCATCCAAGATTTTATCATAAACT
-243

CGTTCAAACCTCCTTTTACCACTCGAAAAGCAATATCTCCGACTTCCTTCAAAGAGAAATGATGACAAAA
-169

CATAGAAACCTCACGTTATACGTTTTGTCATCACGATTTCAGTGCTCACTTTTCTCATTTCATTCTGGCT
-137

TAATTTCATTTTTGTCACTCTCGCGTCATGTTTTGCATTTTTCGAAAGCATTTATTTAAAACTGAAAAAA

TAATTCGTAATTTTTCAAGAATGGCT

FIG. 7

Exemplary M176.1 sequences:

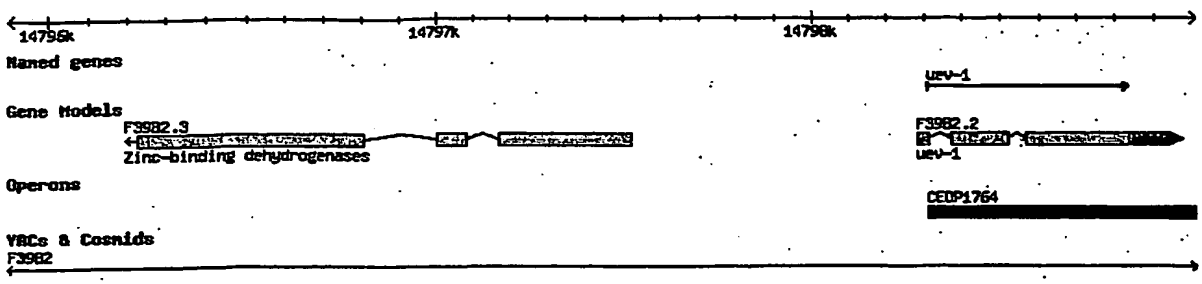
Amino Acid Sequence

MAQKDDRILL LNAPRLPLED DKLNELTADL HDWAHANGLV MRLSTDKLSS EVCQTTPLTL LPSPFPKNVF EEAVHIQNLF
ASLYHFIAYE FDFLIDIHKN VVKTDDFTRN MVEILKKVKA QGLKQPVTLA IQRSDYMCHK DQYSAEYGLK QIEINNIASS
MGAHALRLTE WHIRVLKALN ISDDVIQRAI PENKPIPMIA EALFKAWSHF SNPAAVVLVV VENVNQNQID QRHVEYELEK
LGVPMTCIIR RNLTQCYEQL SLNDRSDLMI DGRQVAIVYF RAGYSPDHYP STKEWEARER MELSTAIKTP WIGLQVANTK
KTQQVLSEDG VLERFIGKPR EARDIRASFA GMWALENTDE VTMKVVAGAQ KHPEAFVLKP QTEGGAALHT GDEMVQMLRE
LPEEERGAFI LMEKLKPMII ENYLVLAKKP ITFAKAVSEL GVYGYAFGRK DAPELKTAGH LLRTKPESTA MGGVAAGHAV
VDTPFLYEFI

Spliced mRNA

aaagaATGGCT CAAAAAGATG ACCGGATTTT GCTGTTGAAT GCTCCAAGGC TCCCGCTCGA AGATGATAAG CTCAACGAGC
TCACCGCTGA TCTTCACGAT TGGGCTCATG CTAATGGGCT TGTCATGCGT CTATCAACCG ACAAGTTGAG CAGCGAAGTT
TGTCAAACTA CTCCATTAAC ACTTCTTCCA TCTCCATTCC CGAAAAATGT TTTTGAAGAA GCAGTTCATA TTCAGAACCT
TTTCGCAAGT CTTTATCACT TCATAGCTTA TGAATTTGAT TTTCTAATCG ATATTCATAA AAATGTCGTG AAAACTGATG
ATTTCACACG GAATATGGTT GAGATCTTGA AGAAAGTCAA AGCCCAAGGA CTCAAGCAAC CAGTCACTCT CGCGATTCAA
CGATCTGATT ATATGTGTCA TAAGGATCAA TATTCAGCGG AATATGGACT GAAACAAATT GAAATAAACA ATATCGCCTC
GTCAATGGGA GCACATGCTC TACGGCTCAC CGAATGGCAT ATCAGAGTTC TTAAAGCGTT GAACATTTCC GATGACGTCA
TTCAAAGAGC AATTCCAGAA AACAAGCCAA TTCCAATGAT CGCTGAAGCT TTATTCAAGG CCTGGTCCCA CTTTTCGAAC
CCAGCAGCTG TGGTTCTTGT CGTTGTAGAA AACGTCAATC AAAATCAGAT TGATCAACGC CACGTGGAAT ATGAACTTGA
AAAGTTAGGA GTACCGATGA CATGTATTAT TAGAAGAAAT TTAACACAAT GCTATGAACA ATTATCATTG AATGATAGAA
GCGATTTGAT GATTGATGGG CGTCAAGTAG CAATTGTTTA CTTCAGAGCA GGATACTCAC CTGATCATTA TCCATCTACA
AAAGAATGGG AAGCACGTGA GCGTATGGAA CTTTCCACCG CTATCAAAAC TCCATGGATC GGGCTACAGG TGGCAAATAC
TAAGAAGACC CAGCAGGTTC TTTCTGAAGA TGGAGTACTC GAAAGATTCA TCGGAAAACC ACGAGAAGCT CGCGATATTC
GAGCTTCATT CGCAGGAATG TGGGCTTTGG AGAACACTGA TGAAGTGACT ATGAAAGTCG TGGCTGGAGC TCAAAAACAT
CCAGAAGCGT TTGTTCTGAA GCCACAAACT GAAGGTGGAG CCGCATTGCA CACCGGTGAT GAGATGGTTC AAATGCTCCG
AGAACTTCCG GAAGAAGAGC GTGGAGCTTT CATTTTGATG GAGAAACTGA AACCGATGAT TATTGAAAAC TACCTGGTTC
TTGCAAAGAA GCCGATCACA TTTGCTAAGG CTGTTAGTGA ACTTGGAGTG TATGGTTATG CATTTGGAAG GAAGGATGCA
CCTGAGCTTA AGACTGCTGG GCATTTGCTC CGAACGAAAC CGGAATCCAC AGCTATGGGT GGAGTAGCCG CCGGACATGC
TGTTGTCGAC ACCCCATTCC TCTACGAATT TATTTGAttt cgaacataat cagaaaactc aacaaaaatg ctgtgatatg
aaaccatttg ctatttagat ctttttgtgt ttgtaaattt aatcattgta atttattgaa tgt

FIG. 8



The F39B2.3 gene is located on chromosome I. Regulatory sequences can be found e.g., in the region between 14 797 521 and 14 798 310. An exemplary sequence of this region is as follows:

CATTTTGAAAGTGCCCAAGTTGCTGGAACGCTGAAAATTGAAATTATTAACAAAGAAATTTGCTTTAAAA

TCCGAAAAATCAAGAAAAAATCGATAATTTCGTCGGACAATCCGCCTGCTAGCACGGCTTGACGCTCGTT

TGCCGCGCGCTCATTCGATTTGTGTGAGTGCCCAGTGGAGCGCGTTTGCTAAGGCTAACTGTGTAGTCCT

CTCGGACAAGATCTGTGAACATTGAAATGAAACACTTGGGTTCAATAAAATCACAAGAAAATGATGACAA
-518

TTTTGTTTGCGACCGAAAAAAAATTATAAAAATTGAATATTGGTTATCATCGTTTCAATCTTTGTTTTGT
-469

ATTAAAGGCACAGCTGCTAAAAATTGTTTTTTTTTTTTCAATTTTGCTAAAAGAAAATCAATTTTCTGAT

TTTTTGTTGAGTTCCCGTGCAAATCAATGTCCTAGCTTTTTAAAATTGTTTTTTGTTATGTAATTCTAAT

CAAATTTTGTCGAATTTTCAGAGATTTTCTGCTAAAACACTAAAAATAGTCTAAAAGTCGATAATTTGAT

AAACATTTACTCAAACCTTTTACGGAAAAATGAAACAAAAGTTGCAAAAATATAGTAATTTCGCAATTTT

CTGAACGCGTACTTAAAGGTACACGGTTTGATTCGGATTGGTCCCGCCACAAAGTGTTACCATAACATTT

TTCTCGCTGCGAGACCCATCCGAATAAATCCGTGCGCCTAATCAGTGCGAGTACGCATTTCATATTACTG

ATAAGTGCCATTTTTAGAACAATG

FIG. 9

Exemplary F39B2.3 sequences:

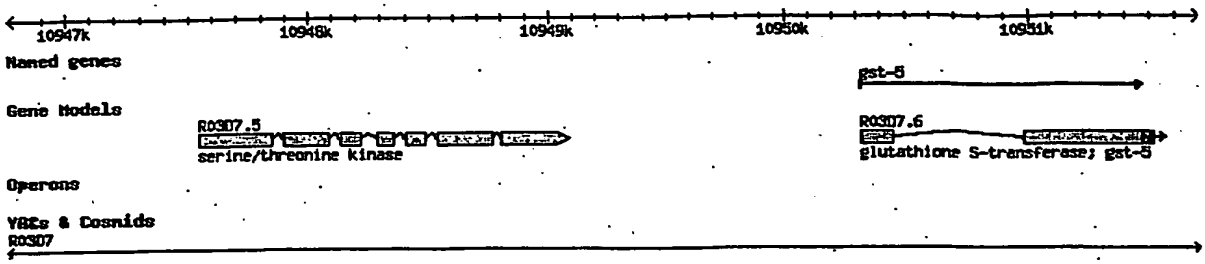
Amino Acid Sequence

MSKSICKSSM RAAVVRRFGA PDVIEAVESD MPRLEKNQVL VRNYAAGVNP VDTYIRAGQY GKLPNLPYVP GKDGAGFVEL
VGESVKNVKV GDRVWYGSEA DSTAEYVAVN RPFELPEGVS FEEGASLGVP YLTAYRALFH LAGAKTGDVI LVHGASGGVG
SALMQLAAWR NIEAVGTAGS ADGIRFVKSL GARNVYNHSD KQYVSKMKND YPGGFNHIFE MAAHTNLNTD LGLLAPRGRV
AVIGNRAETT INARQLMVTE GAVYGVALGM SSEAELLDFG INIVSFLKET EFRPLINKLY RLEQLGLAHE EIMNNKGAKG
NLVVQIEH

Spliced mRNA

ATGAGCAAAT CGATTTGCAA ATCAAGCATG CGCGCAGCTG TAGTCCGACG ATTCGGAGCA CCTGATGTCA TAGAAGCCGT
CGAGAGTGAT ATGCCCAGGC TTGAAAAAAA CCAGGTTCTC GTTCGGAATT ACGCTGCCGG TGTCAATCCA GTTGACACAT
ATATTCGTGC TGGTCAGTAT GGAAAACTAC CAAATCTTCC ATATGTACCA GGAAAAGATG GAGCCGGATT CGTCGAACTT
GTGGGAGAAA GCGTTAAAAA TGTGAAAGTC GGCGATCGAG TCTGGTATGG ATCAGAAGCG GACAGTACAG CAGAGTATGT
TGCGGTGAAT CGACCATTCG AGTTGCCGGA AGGAGTTTCG TTTGAGGAAG GAGCTTCTCT CGGAGTGCCT TATCTTACCG
CTTATCGTGC ATTGTTTCAT CTTGCTGGTG CAAAGACTGG CGACGTTATA CTTGTACACG GAGCATCTGG TGGAGTGGGA
AGTGCACTGA TGCAGCTGGC TGCCTGGAGG AACATTGAAG CTGTTGGCAC TGCTGGATCT GCTGATGGGA TCCGGTTCGT
GAAGAGTCTT GGTGCACGGA ATGTCTATAA TCATTCGGAT AAGCAATATG TGTCGAAAAT GAAAAATGAT TATCCAGGAG
GCTTCAACCA CATTTTCGAA ATGGCTGCTC ACACAAATCT GAACACGGAC CTCGGATTGC TGGCTCCACG TGGTAGAGTT
GCAGTAATTG GAAATCGCGC CGAGACCACG ATCAACGCAA GACAACTTAT GGTTACAGAA GGAGCTGTTT ACGGTGTAGC
ATTGGGAATG TCTTCCGAGG CTGAGCTCTT GGACTTTGGC ATCAACATTG TCTCATTCTT GAAGGAAACC GAGTTTCGTC
CACTTATAAA CAAATTGTAT CGTCTCGAGC AATTAGGACT GGCTCATGAG GAAATTATGA ACAACAAGGG AGCGAAAGGA
AATCTTGTAG TGCAAATCGA ACATTAAttc attattttaa cacgccattt aaaggaa

FIG. 10



The R03D7.6 gene is located on chromosome II. Regulatory sequences can be found e.g., in the region between 10949088 and 10950317. An exemplary sequence of this region is as follows :

AGAACTTTTCGAGAAGTCTACCGTTGTAGTTTTCGAAATAGTAATTTATTTAGTGACGTTTATAAAGGTTTACATGATTT
GGTTTGGAAATTTTTTAGGAGTTTATTCATAAAAACAAAGTAACCATGGACATTCCAGAAGTCTATAGTACACGCGATCC
TACCGTACCCTTCAGTATTTCTATCAGATTGATAGCTTTCGGTAGTCAGGTACAGCCTAAAAAATTCCTGCTTGCCTTTT
TGCCTACATGTCTGCCTACCTTCAGTCATAATGCCTACATAATG
-947

ATTTTTTCCAATTGAAACTTGCAGACAGAAATTCAAATGGCAAAAAGAAACAAACACCGAAACATTAATCA

CATTTCTTTTCATATCAGTTTTCCTGTCAAAGCACATTTCTGGAGTCTGTGTGTATTTTTTTGTGTCTTTATGTGATCGG
TGTTGTGAAATTTGTAGTTGATGTTGATAACATACTTTTTTTTGAAACAAAAAGTGATTGATTAGGCTTGAATTCAGAGA
TATGTTCGTGATACTTTGCGATTCTCGAGCCAAAAACACGGTATCCGGTCTCGACACGACAACTTTTTCGCAAAATACAA
GCTGATGTGCGCCTTGAAAGAGTACTGTAATTTCAACCTTTCGTTGTTGCGGAATTTTCATAGTTTCTGGTTCAAAATAT
ATGTATTTATTAAACAAAAAACTAAAACAAAACAATTGAGAACACATAAATTGTGAAAAATCAATGAGAGCACAGCAAAA
AATTTTGTATCTACAGTACTCTTTAAAGGCGCACATCCGTTCTTATTTTCAGCAAAAATGTCGCTTCGAGACCGGGTACC
GTATTTTTTTTTGTGCAAAACTTTAGGTCTAGGTAATATTAAAAAAAAATTCCACAAAACTAGAATCTAGAGCTTTCCAT
TAAATTTTTTGATGACATTTGAAAATTCATGATGATTTTTTTCCAACAATTTCGAAATATCCCTCTTTTCACCTGGTCC
-302 -282

ACTGAATTCTCTTTCCGAAAGACCACCACAATTTCAGGGCTCCGCCCATTTCGTGGTTTGTAGCCTTCCCGACCCTAGGT
TTTTGATGACAATTGTGAGAGAAGTGAGAGGTTCAGACACAAAAAGCGACGTGGTCGAATGA
-149

GTATAAATAGAGAGTGAAGTTTCCAATTTCCCTCACAATTGTTTGTTTGCAATCCACTTTCCAAAAAAACACAACTTCAA
TCAAAAATCATTATGGTT

FIG. 11

Exemplary R03D7.6 (gst-5) sequences:

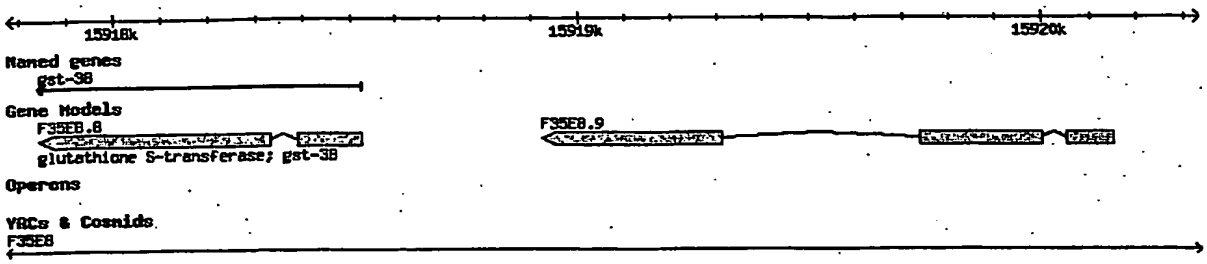
Amino Acid Sequence

MVSYKLTYFN GRGAGEVSRQ IFAYAGQQYE DNRVTQEQWP ALKETCAAPF GQLPFLEVDG KKLAQSHAIA RFLAREFKLN
GKTAWEEAQV NSLADQYKDY SSEARPYFYA VMGFGPGDVE TLKKDIFLPA FEKFYGFLVN FLKASGSGFL VGDSLTWIDL
AIAQHSADLI AKGGDFSKFP ELKAHAEKIQ AIPQIKKWIE TRPVTPF

Spliced mRNA

ATGGTTTCCT ACAAGTTGAC CTACTTCAAT GGACGTGGCG CTGGAGAAGT GTCTCGTCAG ATTTTCGCCT ATGCCGGACA
ACAATACGAG GATAATAGAG TCACTCAGGA ACAATGGCCA GCATTGAAAG AAACCTGCGC TGCTCCATTC GGACAACTTC
CATTCCTCGA AGTCGACGGT AAGAAGCTTG CTCAATCCCA CGCGATTGCT CGTTTCTTGG CTCGTGAGTT CAAGCTCAAC
GGAAAAACCG CCTGGGAAGA GGCTCAAGTG AACTCTCTTG CCGATCAATA CAAGGATTAT TCAAGTGAGG CTCGTCCATA
TTTCTACGCT GTCATGGGAT TCGGTCCAGG AGACGTTGAA ACTTTGAAGA AAGACATCTT CCTTCCAGCA TTTGAAAAGT
TCTACGGATT CTTGGTCAAC TTCTTGAAGG CTTCGGGATC CGGATTCCTT GTCGGAGACT CTTTGACCTG GATTGACTTG
GCTATTGCCC AACATTCAGC TGATTTGATT GCCAAGGGAG GTGATTTCAG CAAGTTCCCA GAGCTCAAGG CTCATGCCGA
GAAGATCCAG GCGATTCCAC AAATCAAGAA ATGGATCGAG ACCCGTCCAG TCACACCATT CTAAatagct gtataaaatc
tgcaaataaa tatttttttt tttt

FIG. 12



The F35E8.8 gene is located on chromosome V. Regulatory sequences can be found e.g., in the region between 15 917 841 and 15 918 925. An exemplary sequence from in or around this region is as follows:

TCTCATTCTCTTCAAGACATAACACAACGGGCTGACGACCATATCATCAACGACGATTTTTTAGGAACTG
TACTTTATCTGTGTCTGACCAACACGTGTGAATGAAGTTTCAACTGGAAAATTTGTTTGAAACACTGCAA
AGAATTTCGAATTTTGATGATAATTTTAAATGCCATTATCAGTTTTAATACGCCACTCTAGTCTTTGATT
-240

CTTTGCACACACACACACACACACACACACACACACACACACTCACAAACACGCCTGAAATTTCGCAATATG
CTGATTTAACGAGAAAACATTTGATGACAATAAACTTGGCGTATTAATATAAAAGGGAAAATTCAATTCA
-94

GATTCTCAACGGTTTATTTTCTGTCACAACTCTTCCTAATATTCACCATGGTTT

FIG. 13

Exemplary F35E8.8 (gst-38) sequences:

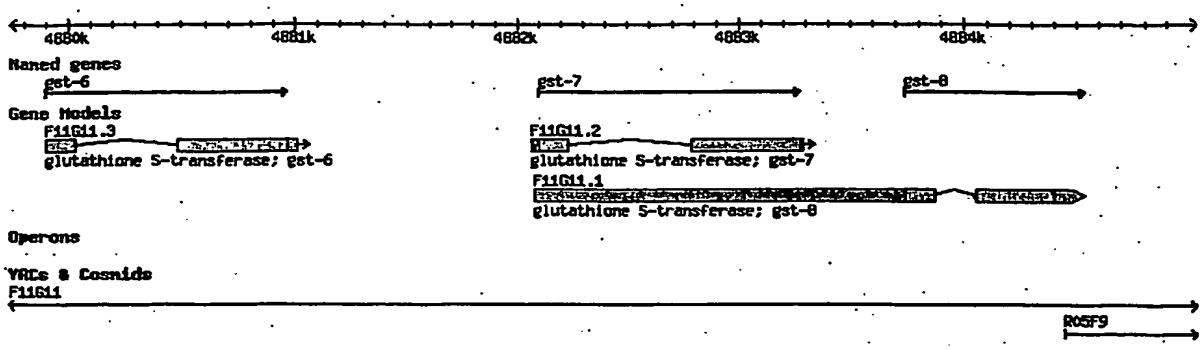
Amino Acid Sequence

MVSYKLTYFD GRGAGELCRQ IFAAAEQKYE DNRLTDEEWE KFKAAGKTPY NQLPMLEVDG KPLAQSHAMA RYLAREFGFN
GKSRWEEAQV NSLADQYKDY YAEARPYLAV KLGYTEGDAE ALYTSVYLPV FKKHYGFFVN ALKASGSGFL VGNSLTFIDL
LVAQHSADLL GREKSDLFND VPEMKAHSEK VQSIPQIKKW IETRPASDW

Spliced mRNA

ATGGTTTCCT ACAAGCTTAC CTACTTCGAT GGACGCGGAG CCGGAGAGCT CTGCCGTCAA ATCTTTGCTG CCGCCGAGCA
GAAATATGAA GATAACAGAC TTACCGATGA GGAGTGGGAG AAGTTCAAAG CGGCCGGAAA AACCCCATAC AACCAGCTTC
CAATGCTCGA GGTAGATGGC AAACCACTCG CTCAGTCCCA CGCGATGGCT CGTTATCTTG CTCGGGAATT CGGGTTCAAC
GGAAAGAGCA GATGGGAAGA AGCTCAAGTC AACTCCTTGG CCGACCAGTA CAAAGACTAT TACGCGGAGG CTCGTCCATA
CCTCGCTGTG AAGCTTGGTT ACACAGAAGG AGACGCGGAG GCTCTTTACA CAAGCGTCTA TCTTCCAGTT TTCAAGAAAC
ACTATGGATT CTTTGTCAAT GCTTTGAAGG CCAGCGGGTC AGGATTCTTG GTTGGAAATT CCTTGACTTT TATTGATTTG
CTTGTTGCTC AGCATTCAGC TGATTTGCTG GGACGTGAAA AGTCGGATCT TTTCAATGAT GTCCCAGAGA TGAAGGCACA
TTCCGAAAAA GTTCAGTCAA TTCCTCAGAT CAAGAAATGG ATTGAGACTC GTCCAGCGAG TGACTGGTAA

FIG. 14



The F11G11.2 gene is located on chromosome I. Regulatory sequences can be found e.g., in the region between 4 880 968 and 4 882 068. An exemplary sequence in or around this region is as follows:

AATTGAAATGAGTTTGCAATTTTGTATTATTTTTTAATTCATATTTCAAGAAGCAATTTTTTGCTAATTTGTTTTAATGG
AAATCGATGTTTCTAAAATATCTTGAATGAATTGTTCTTTTAAAAATTTTATGGTAAAGTTTTCAGCAGGATGTTTCTAT
AGAAGCTTTTTGCATTGCAAGAGTGTTGAAATATACAGGATATTTACAAAAGCCTGGGAAGTAGGCATGCTTTTAGGTAC
AAATCAGACCTACACCGCCTTCCTTTGTGGTTTACCATCATAGCTAAAACTTTCCGAACATTCCCTGGTGAGACACAATG
TTCAAAGCACAAAACCAATCACGTCATAATGTTAATTTGACTTTTATTGTCAAAAATTACAAAAGCGTCGTTTTCTGGAA
CATGAACATAATAAGAATTTTCAAATTTCGGTGGGCACAATAAATATGTAATCTTTTATTTATTTTTGGAGGATAGTCTT
TTCAAAGGCAGGTGTATAACCCTCAAAAGAAAGCACGTTTGTGTTTCAAAGTGAGACTTAAATTATTTCAAAGACAAATT
CCATAGGAAATCATTGTTCATCAGGCACCTTCCCAGAAATTAGGCTGTAGGCAGGCACGTAGGCTGCGGTAAATGCCTAC
GCCTCTTTTGCGCGAGATTATGAAATTGTGTTGTACTGTCGGAAAAATTTCAGAAACAAAAAAAAATATTTTTTGTGACT
TTTTGTGTCAGTTATAGTAGTTTCTTATCATGGTATCTTCAATAATAATGGCAAGCGTAAC
-391

AAGATGATTGATGCCATGGGTTTATATTTGTGAGTAGTCACAAATTGTGACACAACATTCCCTTCGAAAGATCTGGAAAA
GTCACAAAACCTTGCATATATTTTTTTCAACCAATATTATTTTGACCTACTCTGTTCATCGTAACATTGCAACAACAAAA
AACGATGACTACACTTTATGATTTCTAGTCAACAACGTGCGCGCAATGTGTAGAGCAAATGATGACAAACTACAGAATAT
GGTGAGTGGAGAGACGACAGACATTTGAGAAATGGGTATAAATA
-133

GAGACGGCCGGCATTCAGTGTTCAACCCTTCTCATCGACCACTCGATTTCTTGCTTGGTTATTTCAACAATG

FIG. 15

Exemplary F11G11.2 (gst-7) sequences:

Amino Acid Sequence

MVHYKVSYFP IRGAGEIARQ ILAYAGQDFE DNRIPKEEWP AVKPSTPFGQ LPLLEVDGKV LAQSHAIARY LARQFGINGK
CAWEEAQVNS VADQFKDYLN EVRPYFMVKM GFAEGDLDAL AKDVFLPGFK KHYGFFANFL KSAGSGYLVG DSLTFVDLLV
AQHTADLLAA NAALLDEFPQ FKAHQEKVHS NANIKKWLET RPVTPF

Spliced mRNA

cgaccactcg atttcttgct tggttatttc aacaATGGTC CACTACAAGG TATCGTACTT CCCAATTCGT GGAGCTGGAG
AGATTGCTCG TCAGATCTTG GCCTACGCTG GACAAGACTT CGAGGACAAC AGAATCCCAA AGGAGGAATG GCCAGCTGTC
AAGCCAAGCA CTCCATTCGG ACAGCTTCCA CTCCTTGAAG TTGACGGAAA GGTTCTTGCC CAATCTCATG CTATCGCCCG
TTACTTGGCT CGTCAGTTCG GAATCAATGG AAAGTGTGCA TGGGAGGAGG CTCAAGTCAA CTCGGTTGCT GATCAATTCA
AGGATTACCT CAACGAAGTT CGTCCATACT TCATGGTGAA GATGGGATTT GCTGAAGGAG ATCTCGATGC TCTTGCCAAG
GACGTCTTCC TTCCAGGATT CAAGAAGCAC TATGGATTCT TTGCTAACTT CCTCAAGTCG GCTGGATCCG GATACTTGGT
TGGAGACTCT TTGACCTTTG TCGACTTGCT CGTCGCTCAG CACACTGCTG ATCTTCTGGC TGCCAACGCA GCTCTTCTCG
ATGAATTCCC ACAATTCAAG GCTCATCAGG AAAAGGTTCA CTCGAATGCC AACATCAAGA AGTGGTTGGA GACTCGTCCA
GTTACTCCAT TCTAAatgat ttcca

FIG. 16

The K08F4.7 gene is located on chromosome IV. Regulatory sequences can be found e.g., in the region between about 10141800 and 10142217. An exemplary sequence of this region is as follows:

ATTATCCAAAAAGATTAGAAGTTGGCAAACCTTGGGCAAGAATTTCCAGAGATTGCACTAAAGTTGTAGCCAAGTTTGAT
CCAACTTTATCCAATCTTTTACTAAAATTATCCTTAAGACTATTTAAATTTTAGATAGAGAATTGGCGAGAGTTAGATCC
CACTTGGATATGACTTATAGTTAGCCTAACCTGAAGCTATTGCTTGCTTGATCATTTGGTTTATCGCTTTGCTACTTGGA
TAACCAGCTCCAATAGTTGTTATTTTTGCTTTTGTCATCATTTT

-157

TCCACGATTTACACTCTCAAGTGAAACCAACTGTTCTTTGATGCCAGACGATGACATTACACTTGATAAGA

-83

AAATATATATAAACTGGAATTAAAAACAATTGATACATCGATTCAATTACTGAATTCTAATTATG

FIG. 17

Exemplary K08F4.7 (gst-4) sequences:

Amino Acid Sequence

MPNYKLLYFD ARALAEPIRI MFAMLNVPYE DYRVSVEEWS KLKPTTPFGQ LPILQVDGEQ FGQSMSITRY LARKFGLAGK
TAEEEAYADS IVDQYRDFIF FFRQFTSSVF YGSDADHINK VRFEVVEPAR DDFLAIINKF LAKSKSGFLV GDSLTWADIV
IADNLTSLLK NGFLDFNKEK KLEEFYNKIH SIPEIKNYVA TRKDSIV

Spliced mRNA

ATGCCAAACT ATAAGCTATT GTATTTTGAT GCTCGTGCTC TTGCTGAGCC AATCCGTATC ATGTTTGCAA TGCTCAATGT
GCCTTACGAG GATTATAGAG TTTCAGTGGA AGAATGGTCA AAGCTGAAGC CAACGACTCC ATTTGGCCAG CTTCCCATTT
TACAAGTCGA TGGAGAACAA TTCGGTCAGT CAATGTCTAT CACAAGATAC TTGGCAAGAA AATTTGGACT CGCTGGAAAA
ACTGCAGAGG AAGAAGCTTA CGCTGATTCA ATTGTAGATC AATACAGAGA TTTCATATTC TTTTTCCGTC AATTCACTTC
TTCCGTTTTC TATGGAAGTG ACGCTGATCA TATTAACAAA GTACGTTTTG AAGTTGTTGA ACCAGCCCGT GATGATTTCT
TGGCAATAAT CAATAAGTTC CTGGCCAAGA GTAAATCAGG ATTCCTCGTT GGAGACTCAT TGACTTGGGC TGATATTGTG
ATTGCTGACA ATTTGACAAG TCTCCTGAAG AATGGATTCT TAGATTTCAA CAAAGAAAAG AAGTTGGAAG AGTTCTATAA
CAAGATTCAT TCAATTCCAG AAATTAAGAA TTACGTGGCA ACAAGAAAGG ATAGTATTGT TTAAaatcga attatttaag
tctgaattat gtatgtagta aaataatatc gttcctatca cgtctcccag agagcgtaat aaattattat tatgtg

FIG. 18

The *sod-1* gene is located on chromosome II. Regulatory sequences can be found e.g., in the region between about 6 973 806 and about 6 974 406. An exemplary sequence of this region is as follows:

ATTCCGCAACCCCGTCAAATTTAAGAAGAGAAAGAAAAAAAACACAACGTGTTTGCACCTGTAAGGTAGT
TTTTTTTTGTTGCCTTCGGCGTTTTGATTCACATGAAAGTTTCTACGGAAAAACTTTCATTGCATAACGA
TCTTCATATCTTGTTTCTGGAAACGAAAATTTCCAACATGAAAGAAACCCGACGCTATTTATTCTCGCAA
CACAAAAATTTCACATTTAAATAACCGCGGTTTTTCTCGAACAGCATATTTGACGCGCATTGCTCGTCAA
GTTTGATGCGTGCACACTATTTTGCTGTTGTTTTTTTCTTTTTTCTCTAAATTTTCTTTACGCTTTCGTA
GTTTCTATAGAAACGATTCTCCACTCCCGGTTTTCTTCCGATTCTCAAAATTAATTAAAATTTAGTTATT
AAAAATCCTTTTTCTTGAAATAATCGTTCAATTTCGAGTTTTCAAGAGTGGAGACGTTGAATTTGTGAGC
CGCTTATTTTTTCTGTGTTTTTGTTTTGTGGTTTTTAATCAGTGTCATAATCATACTTTCCATTGTTTCT
-64

TTATTATTCAAAGTTGTAGATTCAGTATTTTAGATCGGTGATG

FIG. 19

Exemplary sod-1 sequences:

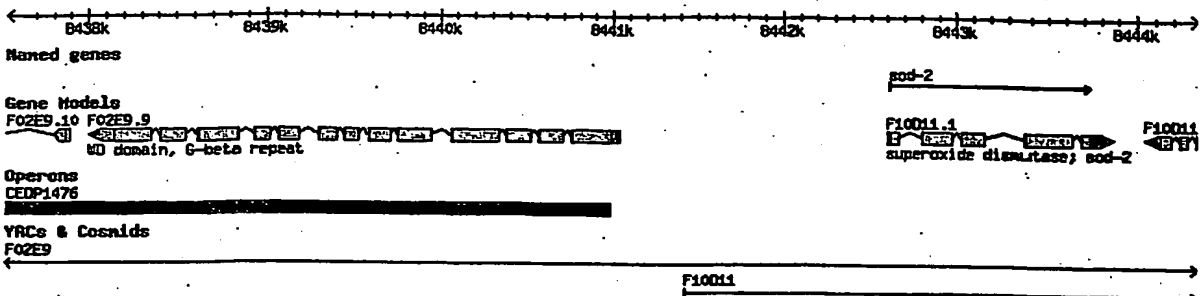
Amino Acid Sequence

MFMNLLTQVS NAIFPQVEAA QKMSNRAVAV LRGETVTGTI WITQKSENDQ AVIEGEIKGL TPGLHGFHVH QYGDSTNGCI
SAGPHFNPFG KTHGGPKSEI RHVGDLGNVE AGADGVAKIK LTDTLVTLYG PNTVVGRSMV VHAGQDDLGE GVGDKAEESK
KTGNAGARAA CGVIALAAPQ

Spliced mRNA

tttagatcgg tgATGTTTAT GAATCTTCTC ACTCAGGTCT CCAACGCGAT TTTTCCGCAG GTCGAAGCCG CTCAAAAAAT
GTCGAACCGT GCTGTCGCTG TTCTTCGTGG AGAAACTGTT ACCGGTACTA TCTGGATCAC ACAGAAGTCC GAAAATGACC
AGGCAGTTAT TGAAGGAGAA ATCAAGGGAC TTACTCCCGG TCTTCATGGA TTCCACGTTC ACCAATATGG TGATTCCACC
AACGGATGCA TTTCTGCCGG TCCACACTTC AATCCATTTG GAAAGACTCA TGGTGGACCA AAATCCGAGA TCCGTCACGT
AGGCGATCTA GGAAATGTGG AAGCTGGAGC CGATGGAGTG GCAAAAATCA AGCTCACCGA CACGCTCGTC ACGCTTTACG
GTCCAAACAC TGTCGTTGGC CGATCTATGG TTGTTCATGC CGGACAAGAC GACCTCGGCG AGGGAGTCGG AGACAAGGCA
GAAGAGTCCA AGAAGACTGG AAACGCCGGA GCTCGTGCTG CCTGCGGTGT CATTGCTCTC GCTGCTCCCC AGTGActacc
tgaatcgcgt ctctgaatct ccacacaatt cctactaaag acaatttttc atttcttgct ttgtcgttat attcttaaga
atcccgttgt tcctactcct actactgtat attttcacat aaaatttctt caaaatttca aataaaggtt gtagtttc

FIG. 20



The *sod-2* gene is located on chromosome I. Regulatory sequences can be found e.g., in the region between about 8 441 038 and 8 442 612. An exemplary sequence of this region is as follows:

TGAATAAAAACGTTGAACCCAACGGACATCAAAGTATCAAAGTAAGTAAGTAAGTAAGTAACCTGAATAAAAACGTTGCA
TATAAAAAATCTACTCGAAAATTAAGTGAGAATTGAAGGATTGCTTTCCGAAGAGAAAATGACAATTATAGGGTATACTA
AAACATCAAAAATGTATATTAGACTACCATAAATATAAAACATCAGTGCTGCTCTCCAAGCTATTCTGACGGATTGCGAC
AACGAGCTCGCTGGAGTTGGCATCAGTGTGGAAGGCAGACACATAAGAAGACTCGAATTTGCGGATGACGTAGTCCTGAC
ATGTTCCACACCGGGAGAAGTTCAAGAACGACTGGAAATTTTGGACCGAATAAGTTCTAATTACGGACTCAAGATCAATC
AGTCAAAGACTGTTCTTCTGAAGAACAAGTTTTGCCGGAGCCAAGACGTCCTTTTCAACGGATCCCCCATCATTCCCGTG
CCTGGTTGCCGCTATCTGGGTCGCTGGATCGACATTTCTGGCTCAATTGACGAAGAGATCTCGAGGAGAATAAGAGCAGG
TTGGGGTGCTCTGGTTGGAATCAAAGAAGTCTTGAGAATCATGCCAAACAAGGAAAGAATCATCCTCTTCAAGCAAAAT
-980 -959

GTGCTACCAGCTCTCCTGTATGCTAGTGAAACTTGGACTTGTAATGCTGGATCCACGTTGAGACTCAAAAGAACTGTCAC
CGGTCTCATCGACGCTGCAGAAATTCGAGGCTGGAACTTCAACTTGGAACGTTACCTCCTTGCAAAACAATCAAGATTTG
CAGGACACATTCTACGGAGAGATCCAAACCGATGGACAAAAATCTGCACGGAATGGGACCCGAGCCACAACAAAAATTGG
AAACGTGCCGTTGGAGGACAGAAGAAGAGATGGGCTAAGGACATCGACGAAGAATACGCAAAATTCCACCACAATTCCGC
CATGTCGGGACAAGTCGTTGTTGGGAGAAGAAGACTAGGAATGCTCACTCCGAAGGCTCCATGGCTGTCCATCGCACGAA
CCGACCGTGAAAAATGGAAAGAGTTTGTCCGCAGTTGCCTCGCAACTTGAACCCAACGGACATCAAAGTATCAAAGTAAG
TAAGTAAGTAAGTAACCTGAATAAAAACGTTGCAATTAAAAAATCTACTCGAAAATTAAGTGAGAATTGAAGGATTGCTT
TCCGAAGAGAAAATGACAATTATAGGGTATACTAAAACATCAAAAATGTATATTAGACTACCATAAATATTACGATAAT
-363

TTAAAAATTACTAGAAACACGCAATTCGGCTCAAAAAGCAACAATTTAGACTGAAAACGAGCTAAAAGAATATTATTCAA
AAACCACTTTGCTCGGTAAATCTGGTGTATCATGTTCCGCAAACACTGTCTTTTGTTTTGCG
-191

TACTTTGTTTACGCGCATTCGAATTTCAGTGTTCGCGCTTTTTGTTTACTTTTTTATTTTTCATCCAAAAATCGTATTTT
CAGCTTGATATGTTTCTGCGAATTGTAAAAATTTATATTTGACTATTGAATATTTTAATTATTTGCAGCCGAAAATG

FIG. 21

Exemplary sod-2 sequences:

Amino Acid Sequence

MLQNTVRCVS KLVQPITGVA AVRSKHSLPD LPYDYADLEP VISHEIMQLH HQKHHATYVN NLNQIEEKLH EAVSKGNVKE
AIALQPALKF NGGGHINHSI FWTNLAKDGG EPSAELLTAI KSDFGSLDNL QKQLSASTVA VQGSGWGWLG YCPKGKILKV
ATCANQDPLE ATTGLVPLFG IDVWEHAYYL QYKNVRPDYV NAIWKIANWK NVSERFAKAQ Q

Spliced mRNA

tttgcagccg aaaATGCTTC AAAACACCGT TCGCTGTGTC TCAAAGCTTG TTCAACCGAT CACAGGAGTC GCTGCTGTTC
GCTCGAAGCA CTCGCTGCCA GATTTACCAT ACGACTATGC TGATTTGGAG CCTGTAATCA GTCACGAGAT TATGCAACTT
CATCATCAAA AGCATCATGC CACTTATGTG AACAATCTCA ACCAAATTGA GGAAAAGCTT CACGAGGCGG TCTCCAAAGG
AAACGTCAAA GAAGCTATCG CTCTTCAGCC AGCTCTCAAG TTCAATGGAG GAGGACATAT CAACCACTCC ATCTTCTGGA
CTAATTTGGC AAAGGACGGA GGAGAACCAT CGGCGGAGTT GCTCACCGCA ATTAAGAGCG ACTTCGGATC TCTGGATAAT
CTTCAAAAAC AGCTTTCGGC ATCAACTGTC GCTGTTCAAG GATCAGGATG GGGATGGTTG GGATACTGTC CAAAGGGAAA
GATCTTGAAG GTTGCCACAT GTGCCAATCA GGATCCACTT GAGGCAACAA CTGGACTTGT TCCACTGTTC GGAATTGACG
TCTGGGAGCA CGCTTACTAC TTGCAGTACA AGAATGTTCG ACCAGATTAT GTCAATGCTA TTTGGAAGAT CGCCAACTGG
AAGAACGTCA GCGAGCGTTT TGCAAAGGCA CAGCAATAAa tgagctgaat cacaagaatt aatcgtcaaa tgtagcagta
gaagttgact cccattgttt tgtaactatt tttgtttctt aattatttcg aaatgtaaat tttcaaacct tttcaaatga
aaagttttca ccg

FIG. 22

The *ctl-1* gene is located on chromosome II. Regulatory sequences can be found e.g., in the region near 14 306 135. An exemplary sequence of this region is as follows:

AAAAAAAAATCGATAAAAAATCCGCGTCAACGAAAGTTTAAAGTTACAGTATTTGTCGTTTCGAGACCGG
GTACCGTAGTTTTTGGTGAAAACATTGCAAAATTTGGTCAACAATTTCATCGCTGCGAGACCGACACAAC
ACTTTATTTTATTTTTGGGTTTCCCTTATCGCTTATCATAAACATGTGACGTCATCATCTCTTGTACAGA
-997 -978

GCACCGCGACTGGGAGTATAAGAATCGCCGGAAAACATCAATAATCAGTTCGGTAGAAGTGAAAATTGAG
CGTAAAATATGATCATTTTTCGATGCACCATATTTGACGCGCAATACTTCTACAAGCCGCTGTGTACTGC
-880

TCGTGGACAACTTTGGATTATTTTTTGTTTTTAAAATTCAAAATAGTCAATATATTGCTTATTTATAGCG
CGCCTTTTTGACAGTAAGTTTGTCAAATTTGCGCGTAAGTTATGGTGTTTGCACATATGCACCATACAGC
AACACCCCGCGGCCCGGCTAGTGGTACATCCATGCAAATGCGCTCTACTGATAATTTGAGTTTAACCAGG
TTTAGGCGCAAGATAAGAAAAAAGCTTTGGACCAAAAAATTTAGAGTTTATTTTTTTCGGACATTTTTTA
TATACATCACAAAAATATTGGGCCACTCGTTTTTGATAAAAACGACAAGCCCAAAAGTTCAGGTATACGG
TAGACAAATTGCGTACAGGTACCACTTTTCCACGTAGTGCCAGGTTGTCCCATTACGCTTTGATCTATGA
AAAATGCGGGAATTTTTCGTCCAGAAAAATGTGACGTCAGCACGTTCTCAACCATGCGAAATCAGTTGAA
AACTCTGCGTCTATTCTCCCGCATTTTTTGTAGATCTGTAGATTTGTAGATCAATCCATTCCCCGTATAC
CCTGACCCATAATCAATACCTACCTAATTTTTGTCTTTCCCCCTACTTTTTTGCCTGTCCAAAATAAGCG
AGACTATGCCGTAGTCTGGTGTCCAACAACATGTTCCTTATCAGTGATAACGCTACAATCTTCTTTCTTT
TTTCTCTGTTTCTCTTGTCTCTCCCAACCCATATTCCGTATTACACCTCGTCGTGGTCATTTTTTTGTTC
AGAGTTTTATTTAATTCTAAATTTCCTAACTAAAATTTCAGA

FIG. 23

Exemplary ctl-1 sequences:

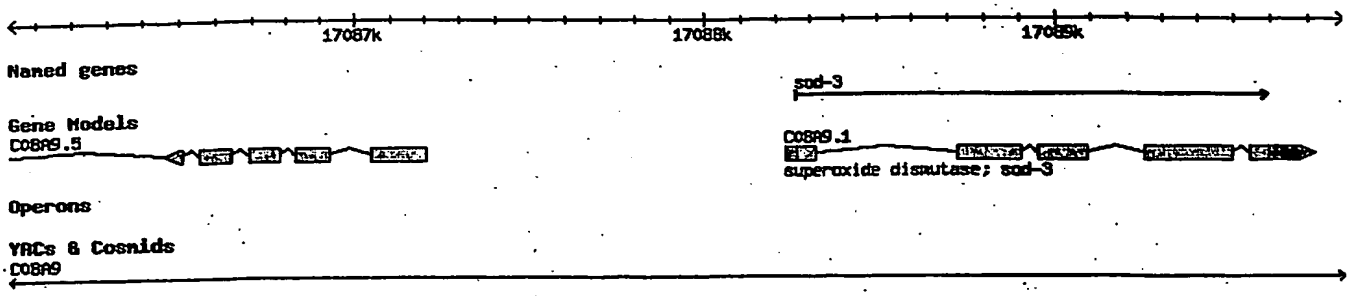
Amino Acid Sequence

MPNDPSDNQL KTYKETYPKP QVITTSNGAP IYSKTAVLTA GRRGPMLMQD VVYMDEMAHF DRERIPERVV HAKGAGAHGY
FEVTHDITKY CKADMFNKVG KQTPLLVRFS TVAGESGSAD TVRDPRGFSL KFYTEEGNWD LVGNNTPIFF IRDAIHFPNF
IHALKRNPQT HMRDPNALFD FWMNRPESIH QVMFLYSDRG IPDGFRFMNG YGAHTFKMVN KEGNPIYCKF HFKPAQGSKN
LDPTDAGKLA SSDPDYAIRD LFNAIESRNF PEWKMFIQVM TFEQAEKWEF NPFDVTKVWP HGDYPLIEVG KMVLNRNVKN
YFAEVEQAAF CPAHIVPGIE FSPDKMLQGR IFSYTDTHYH RLGPNYIQLP VNCPYRSRAH TTQRDGAMAY ESQGDAPNYF
PNSFRGYRTR DDVKESTFQT TGDVDRYETG DDHNYEQPRQ FWEKVLKEEE RDRLVGNLAS DLGGCLEEIQ NGMVKEFTKV
HPDFGNALRH QLCQKKH

Coding

aaaATGCCAA ACGATCCATC GGATAATCAA
CTGAAAACCT ACAAGGAGAC GTATCCAAAA CCCCAAGTGA TCACAACTTC AAATGGAGCT CCGATCTACT CGAAGACCGC
CGTGCTCACC GCCGGGCGGC GTGGCCCAAT GCTCATGCAA GATGTAGTTT ATATGGATGA GATGGCTCAT TTCGATCGTG
AACGTATCCC CGAGCGTGTC GTTCATGCCA AGGGAGCCGG AGCCCATGGA TACTTCGAGG TCACCCATGA CATCACCAAG
TACTGTAAGG CCGATATGTT CAACAAGGTC GGAAAACAGA CACCACTTCT CGTTCGTTTT TCAACGGTCG CTGGAGAATC
GGGATCCGCT GATACTGTCC GCGATCCACG TGGATTCTCT CTCAAATTCT ATACCGAGGA GGGTAACTGG GATCTGGTTG
GAAATAACAC TCCGATCTTC TTCATTCGTG ACGCAATCCA CTTTCCGAAT TTCATTCATG CCCTGAAGCG CAATCCACAG
ACTCACATGA GGGATCCGAA TGCGCTCTTC GATTTCTGGA TGAATCGCCC TGAATCCATT CATCAGGTGA TGTTCCTCTA
CTCGGATCGT GGAATTCCTG ATGGATTCCG TTTTATGAAT GGATACGGAG CGCATACTTT CAAGATGGTC AACAAGGAGG
GAAATCCGAT TTATTGTAAA TTCCATTTCA AGCCTGCTCA AGGTTCCAAG AATCTCGATC CAACTGACGC TGGAAAGCTC
GCCTCTTCGG ATCCAGACTA TGCGATCCGC GACCTGTTCA ATGCCATTGA GTCAAGAAAT TTCCCGGAAT GGAAGATGTT
CATTCAAGTG ATGACATTCG AACAAGCTGA GAAATGGGAG TTCAATCCAT TTGATGTCAC TAAAGTTTGG CCACACGGTG
ATTACCCACT GATCGAGGTC GGCAAGATGG TGCTGAACAG GAATGTGAAG AATTATTTCG CTGAGGTCGA ACAAGCCGCC
TTCTGCCCGG CCCACATCGT CCCAGGAATC GAGTTCTCGC CAGACAAGAT GCTCCAAGGG CGTATCTTCT CCTACACGGA
CACGCATTAC CATCGCCTTG GACCAAACTA CATTCAGCTT CCAGTCAACT GCCCGTACCG CTCCCGTGCT CATACCACTC
AACGCGATGG TGCAATGGCT TATGAAAGCC AGGGAGATGC GCCGAATTAC TTCCCGAACA GTTTCCGCGG ATACCGTACT
CGTGATGATG TGAAGGAGTC GACATTTCAG ACGACTGGAG ATGTTGATCG TTATGAGACT GGAGACGATC ACAACTACGA
GCAGCCACGT CAGTTCTGGG AGAAAGTGCT CAAGGAGGAG GAGAGAGATC GGCTCGTTGG GAATTTGGCT AGTGATTTGG
GTGGCTGTTT GGAGGAAATT CAAAATGGAA TGGTCAAAGA GTTCACGAAA GTTCATCCGG ATTTCGGAAA TGCTCTTCGC
CATCAGCTCT GCCAGAAGAA GCATTAAatt

FIG. 24



The *sod-3* gene is located on chromosome X. Exemplary regulatory sequences include:

TATTCGCAGAAAAAAGTCGTTGCAAACATTCGTTTTTATATGTTTTTCTTTGAGAAAGCGTGGTTCATTT
TTGAAAGTGAAAAATATTTGCTTAAAACTTCCAAATTTAAATCTGCAGTGATTCAGAGAGGTTGAGAATT
ATTTTCAAAAACATTCAATGTTTTCCCTTGGAGTGACTATGCAAATATGAAAATGTTTTCCAAAAATATT
TGGATGCCCTGATAAAAAGTAGGTGAAATTTCGCAGGGGAACATCATATTAAAATGTTGAATTTTTAGAA
GAAATGGAAATGTTTGTCGGTGGTATGCTCGAATATTTGAGATATTATATATTTACTGTTAAATCCGAAA
TTTTTGACAAACGGAAAAAATTTGTGTCGAAATACTACATTTTCGATAACACAAAGGTACTTCCATAACA
CTTATAAAAACTGTTTGACTATCTTATTTCAGGAAAAAAAAATCCAAGAATAAACATTTTTCAGAATTTG
AACTTTCTAATGGCTGATTAATAAAACAAAGTTATACAACTATTCAAAGCAGTTGCTCAATCTGGCATTT
TCTTGTGTTTTTTTTTGAATATTTCATCAGCAAGATGTTGATAATTTTGTGTTAATTCTAATTGTTTTCT
ACAATTTTTCAAACCGAAAATTGACCTTTGACTTTGTTTACTTTGTTCTCGTGGGTTAACTGTTCACTGA
TTTCTATTGCTGTTGATGAGGTCTTTGATCAAATTTGTATTGTTTTTATACTGCATATTGCTTCAATTCT
AAATCATCTAATATATTGTCAAACAACTTCTTGTTTTTTTTTTCATTCAAAACTTCTGCAAAAACGTTCT
-287

CTTAACAAAGGTTCACACAACAACTCTCCTCTCCATCTCTTTCTCTCAACAACAATGTGCTGGCCTTGCA
TGTTTGCCAGTGCGGGTTGTTTACGCGTTTTCAAGATTTTTGGTCTCCTATCTAACGTCCCGAAATGCAT
TTTTTCCTTTCATTTGGTTTTTTTCTGTTCGAGAAAAGTGACCGTTTGTCAAATCTTCTAATTTTCAGTG
AATAAAATGCTG

FIG. 25

Exemplary sod-3 sequences:

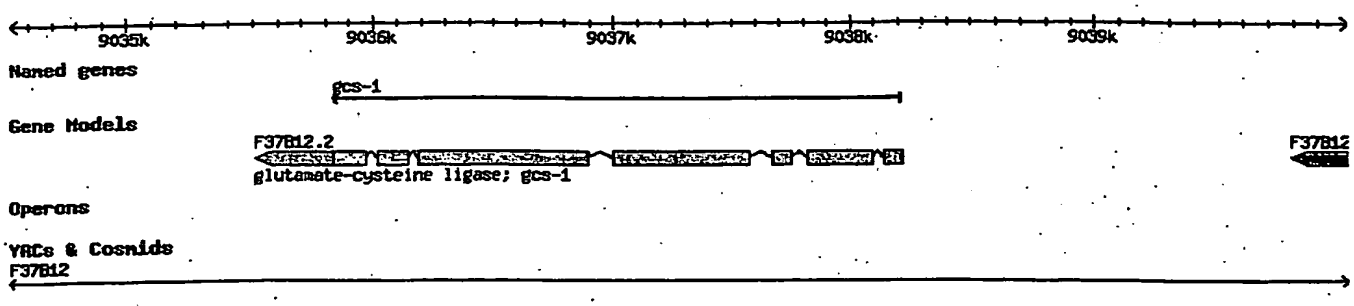
Amino Acid Sequence

MLQSTARTAS KLVQPVAGVL AVRSKHTLPD LPFDYADLEP VISHEIMQLH HQKHHATYVN NLNQIEEKLH EAVSKGNLKE
AIALQPALKF NGGGHINHSI FWTNLAKDGG EPSKELMDTI KRDFGSLDNL QKRLSDITIA VQGSGWGWLG YCKKDKILKI
ATCANQDPLE GMVPLFGIDV WEHAYYLQYK NVRPDYVHAI WKIANWKNIS ERFANARQ

Spliced mRNA

cgtttgtcaa atcttctaat tttcagtgaa taaaATGCTG CAATCTACTG CTCGCACTGC TTCAAAGCTT GTTCAACCGG
TTGCGGGAGT TCTCGCCGTC CGCTCCAAGC ACACTCTCCC AGATCTCCCA TTCGACTATG CAGATTTGGA ACCTGTAATC
AGCCATGAAA TCATGCAGCT TCATCATCAA AAGCATCATG CCACCTACGT GAACAATCTC AATCAGATCG AGGAGAAACT
TCACGAGGCT GTTTCGAAAG GGAATCTAAA AGAAGCAATT GCTCTCCAAC CAGCGCTGAA ATTCAATGGT GGTGGACACA
TCAATCATTC TATCTTCTGG ACCAACTTGG CTAAGGATGG TGGAGAACCT TCAAAGGAGC TGATGGACAC TATTAAGCGC
GACTTCGGTT CCCTGGATAA CTTGCAAAAA CGTCTTTCTG ACATCACTAT TGCGGTTCAA GGCTCTGGCT GGGGATGGTT
GGGATATTGC AAGAAAGACA AAATCTTGAA GATCGCCACC TGTGCAAACC AGGATCCTTT GGAAGGAATG GTCCCACTTT
TTGGAATTGA CGTTTGGGAG CACGCCTACT ACTTGCAGTA CAAAAATGTC CGCCCAGACT ATGTCCATGC TATTTGGAAG
ATTGCCAACT GGAAGAATAT CAGCGAGAGA TTTGCCAATG CTCGACAATA Aaagcaggaa atattggaat tttcggtttt
acgaaaatat tgaagataat tcagatgtag tttaaaacgc tgagaatttg tatttttgta attgtttaaa taaaagaacg
cacagttttt tctta

FIG. 26



The *gcs-1* gene is located on chromosome II. An exemplary regulatory sequence is:

TTATCAACCACTAGGTTCCGTCTTAATCGTCCAAATATTGATCCGCTCGCTCGTGTTTTCTCAACTTCTTTATTTGCTGT
GTTTTTCTGTTTCTATAGTTCTCCATTTTCCATCTCCTCTTCGCTTGTTGAATGGACTTTATTTTGATAAGTTCATTTTA
ATTTTTCTAACAATCTCATCACTAGCTCATGATGACAATTGCAAAGAAATTCGTCATATAGAGGGGAAAAATGCTGACAA
-607

ATATTGAAAAGCCTTCAGGAGAGATGTAGAGACGTAGGAGTAGAGACAGAACATAAATTTGAGAAGCTTGTAGGGAGAAT
AGACATAGAGTTACCATGGGAAAAACGCTCGCATTTTCCATTTAACGAGATTTTCTAGATCACAACATTTTGTGATCCGT
TGTGCGAAAATCAAGCTTTTTATCAAACTTTTATCGTCTGTTCATTCTTTCTGACAATCTTTATTATCTTATTAAACTTG
ACTAATTGTATTGAAAGTATTTTTTTAGATGCGAACGAAGTTCCATTTTTCATGACTTAACATCTCTTAACGTTAGTGAA
-316

ATTTTTGAATTCCAATTAGGACTACGGTAGGAGTTCTGTAGTTGATTTCCTGAACACTTGTTTTGTAACCTTTCTGAACG
GATTTTAATATTTCTAAAATTTTAAATTGCAAATCTGAGTCCTATTAAAAGATGTTTCATCCGTAAAACCAACAAACAAA
ATATCACTTTATCATCATGAGATTTAATGTTTCCTTTTGATTTTCTGAATTGTTGTACTTTCCTTCAAACGACTTATTGA
-121

ACTGATGTAACTTTCCTTCTAATGTTATCATTTGTATTTTTTTGCAGAATG

FIG. 27

Exemplary gcs-1 sequences:

Amino Acid Sequence

MGLLTKGSPL TWAETVPHID YIKKHGIAQF INLYHRLKSR HGDQLKWGDE IEYTIVKFDD ANKKVRVSCK AEELLNKLQA
EEQVNAMLGT ANRFLWRPEF GSYMIEGTPG MPYGGLIACF NIVEANMKLR RQVVKKLLKK DETCLSISFP SLGVPGFTFP
EVAADRKNDD AANSVFWPEQ AVFLGHPRFK NLTKNIKGRR GSKVAINVPI FKDTNTPSPF VEDLSALGGP DDTRDAKPDH
IYMDHMGFGM GCCCLQVTFQ AVNVDEARWL YDQLTPITPI LLALSAATPI FRGKLSNVDS RWDIISASVD DRTPEERGLE
PLKNSKWVID KSRYDSTDCY IYPCSVGYND IPLQYDETIY KQLIDGNIDE PLAKHIAHMF IRDPHQVFRE RIEQDDEKSS
EHFETIQSSN WMNMRFKPPP PDAPEIGWRV EFRPTEVQLT DFENAAYCCF VVLLTRMMIS FRLTYLMPIS MVTENMKRAQ
QKDAVLNQKF LFRKGLAECK SAPENLKGSE KCGPPSQDIE EMSIDEIING KKNGFPGLIS LIRQFLDSAD VDVDTRCTIS
QYLNFISKRA TGEINTLAHW TRGFVQSHPA YKHDSDVNDN IVYDLLKKMD AISNGEDHCE KLLGCYRSKT DHAISAAVRK
AEEHMIVSSQ KRAH

Spliced mRNA

tttgcagaAT GGGTCTTTTG ACGAAAGGTA GTCCGTTGAC GTGGGCAGAA ACCGTACCGC ACATTGATTA TATCAAGAAG
CACGGAATTG CTCAATTCAT CAATCTCTAC CATCGTCTGA AATCAAGACA CGGAGATCAA TTGAAATGGG GAGATGAGAT
TGAATACACT ATTGTAAAAT TTGATGACGC AAACAAGAAA GTTCGCGTGT CGTGCAAAGC TGAAGAGCTT CTTAATAAGT
TACAAGCCGA AGAGCAGGTG AATGCGATGC TTGGAACTGC CAATCGATTC CTTTGGAGAC CAGAATTCGG ATCCTACATG
ATCGAGGGAA CCCCCGGAAT GCCTTACGGA GGTCTCATCG CTTGCTTCAA CATTGTCGAG GCAAACATGA AATTGCGCAG
ACAGGTCGTC AAAAAGTTAT TAAAGAAGGA TGAAACATGT CTATCGATAT CGTTCCCATC TCTTGGAGTA CCTGGATTCA
CATTCCCGGA AGTAGCAGCT GATAGAAAGA ATGATGATGC AGCTAATAGC GTTTTCTGGC CAGAACAAGC TGTATTCTTG
GGCCATCCAC GTTTCAAGAA TCTTACCAAA AATATTAAAG GTCGCAGAGG AAGTAAAGTA GCTATCAACG TCCCGATATT
CAAGGATACG AACACCCCCA GTCCATTCGT TGAAGATTTA TCTGCACTTG GAGGTCCTGA TGATACTCGT GATGCGAAAC
CTGATCACAT TTATATGGAT CATATGGGAT TCGGAATGGG GTGCTGTTGT CTTCAAGTCA CTTTCCAGGC TGTGAACGTC
GATGAAGCCA GATGGTTGTA CGATCAGCTG ACACCGATTA CACCGATTCT ACTGGCACTC TCTGCCGCCA CACCAATCTT
CCGTGGAAAA TTATCCAATG TCGATTCTAG ATGGGATATC ATTAGTGCAA GTGTCGACGA TCGTACACCG GAGGAAAGAG
GATTGGAACC TCTCAAGAAT TCGAAATGGG TTATTGATAA GAGTCGCTAC GACTCCACGG ACTGTTACAT TTATCCATGT
TCTGTTGGCT ACAATGATAT TCCTCTTCAA TACGACGAAA CCATATATAA ACAACTAATT GATGGAAATA TTGATGAGCC
ACTGGCAAAA CATATTGCGC ATATGTTCAT TCGTGATCCA CATCAAGTTT TCCGTGAGCG TATCGAACAG GACGATGAGA
AAAGCAGTGA ACACTTTGAA ACAATTCAAT CATCGAATTG GATGAACATG CGATTCAAGC CACCACCACC AGATGCTCCA
GAAATCGGAT GGAGAGTCGA ATTCCGGCCA ACTGAAGTTC AACTGACCGA CTTTGAAAAT GCAGCATACT GTTGCTTCGT
TGTATTGCTC ACCAGAATGA TGATCTCCTT CAGGCTGACA TATTTGATGC CAATTTCAAT GGTTACTGAA AATATGAAGC
GTGCTCAGCA AAAAGATGCA GTTCTCAATC AGAAATTCCT GTTCAGAAAA GGATTGGCTG AGTGCAAATC TGCTCCCGAA
AATTTGAAAG GATCGGAGAA ATGTGGACCA CCTAGTCAAG ATATTGAAGA AATGTCGATT GATGAGATTA TCAATGGAAA
GAAAAATGGA TTCCCAGGTC TCATTTCACT TATTCGCCAA TTTCTAGATT CTGCTGATGT TGATGTGGAT ACTCGGTGTA
CGATTTCTCA ATATTTGAAC TTTATTTCGA AACGAGCAAC TGGAGAGATT AATACTTTGG CTCACTGGAC ACGTGGATTC
GTACAATCTC ATCCTGCATA CAAACATGAC AGTGATGTAA ATGATAATAT AGTTTACGAT CTTTTGAAAA AGATGGATGC
CATCTCAAAC GGAGAAGATC ACTGTGAGAA GCTGCTCGGA TGCTACCGCT CTAAAACCGA TCATGCCATT TCTGCTGCTG
TTCGCAAAGC TGAAGAGCAC ATGATCGTGT CCAGCCAAAA ACGTGCACAT TAGgcgataa ttgattgatt atgtgatttt
aatttattta tgttctatac gtcgtgtttc ccattccttc taggccttcc atgattcaca atttttcgat gccatatcaa
tttagttggc catctacatt aaattactga tatgttgatg ctattttcta gtaagcagat gtcagtgttt agtaattcaa
aaatttaaac tctgaatttc taaatgcttg ttttttgagt agtaggaatc agtacgaatg gtacattaat ctgaaaataa
tttcatattt atgtacaatg ctcccctgaa tccatcatat aattattatc cgtgttg

FIG. 28

T19E7.2c (spliced)

aatcgttctt cttcttattt tctacagctg atgatgtttg atgaaggttt tattttcctt gctttttcca
ccctgttaat attattttcg atattcccaa aaataattcc aaattttcag tccatattca tctggatact
tgcaacatca tcactgattt tggtgatcag ttcaccatcg tccaacacct caatccaatc atcgtcatac
gatcggatca cgacaaaaca tcttctggac aatatatcac cgacatttag tgagtatgac ttgaaaagtg
catctgatca cttttcgagc cgttttgtcg ctagggactt tttaatgaat cagatgtact tttcgaattt
tttagagcaa aagcagtagt tgcacttttg aaacttaaat taatatacaa aactatgata tatattttca
gaaATGTACA CGGACAGCAA TAATAGGAAC TTTGATGAAG TCAACCATCA GCATCAACAA GAACAAGATT
TCAATGGCCA ATCCAAATAT GATTATCCAC AATTCAACCG TCCAATGGGT CTCCGTTGGC GTGATGATCA
ACGGATGATG GAGTATTTCA TGTCGAATGG TCCAGTAGAA ACTGTTCCAG TTATGCCAAT ACTCACCGAG
CATCCACCAG CATCTCCATT CGGTAGAGGA CCATCTACAG AACGTCCAAC CACATCATCT CGATACGAGT
ACAGTTCGCC TTCTCTCGAG GATATCGACT TGATTGATGT GCTATGGAGA AGTGATATTG CTGGAGAGAA
GGGCACACGA CAAGTGGCTC CTGCTGATCA GTACGAATGT GATTTGCAGA CGTTGACAGA GAAATCGACA
GTACCG[illegible]
[illegible] CAATAACAAT CAATATCAGC AGAAACATCA GCAACAACAG [illegible]
AACTGTTGAA CATGCAACTG AAAAAGCCGA ATTGCAAGAT GATGTGTTTG [illegible]
TTGCAGGATG TTTCAAGACA AGAATCACAA TTGAATCAAC TTTTTGATAA TAAGCAA[illegible]
[illegible] TTTATAATCA GCGAAATTTG ACCGAGATGC AAGAGATGCC
TGATTCCTGC AATCAAGTTT CCATTTCAAC AATTCCAACA ACATCGACTG CTCAACCAGA GACTTTGTTC
AATGTAACCG ATTCACAGAC TGTCGAACAG TGGCTTCCAA CAGAAGTTGT ACCAAACGAT G[illegible]
[illegible]
[illegible]
[illegible]
[illegible] TGATTCGTCA TCAACGTGCT CTCGCCTCTG
TTCGGAATCT CCACGATACA CGTCAGAGAG CTCAACCGGA ACTCAGGAGT CTCGTTTCTA CGGAAAGTTG
GCTCCATCCA GTGGATCACG CTACCAACGA TCATCGTCTC CACGTTCATC ACAATCTTCC ATTAAGATCG
CGAGAGTTGT TCCACTGGCC AGCGGACAAC GGAAGCGTGG ACGTCAATCC AAGGATGAGC AGCTCGCCAG
TGACAACGAG CTTCCAGTGT CGGCGTTCCA GATTTGGGAG ATGTCATTAA GCGAGTTGCA ACAAGTGTTG
AAGAACGAGA GTCTCAGCGA GTATCAAAGA CAGTTGATTC GCAAGATTCG TCGACGCG[illegible]
[illegible]gaagc
cctcttttat cacataaaat ctcggtcgaa accttattaa agccacataa ttaaagataa ttaattccgc
cacaataatc gtttttttct tctttgccgt gtctcatttc attttgatct actctttcct cccttcggat
tctttgattt cccagtgaaa tacctcaccc acttcaatcc ccacaaagtg agcaacccct atcttgcaac
agttttatca tctcttcatc atacccagtt tgataattta ttatctgatc cccatcccct tgtcgcctct
cattagtatc ctagtttttc atttgagccc ggagctcaga ctacatctcc gaatcatcat acaaatagat
agaaacgggt ctcgtgacga aagaatacgt gcaccacacg acccccccat cctgttcacc cccatacacc
tgaaaaatat gatctttaca gttatttcta ttatatcctc aaatctctcg taatatcgta tcaatttcct
cttctttttt gtcattttca atttttctca aatttctcag atctattctt tttcttgtat ttttggaact
tgtatccctc ctccatcccc agact

T19E7.2c (conceptual translation)

MYTDSNNRNF DEVNHQHQQE QDFNGQSKYD YPQFNRPMGL RWRDDQRMME YFMSNGPVET VPVMPILTEH
PPASPFGRGP STERPTTSSR YEYSSPSLED IDLIDVLWRS DIAGEKGTRQ VAPADQYECD LQTLTEKSTV
APLTAEENAR YEDLSKGFYN GFFESFNNNQ YQQKHQQQQR EQIKTPTLEH PTQKAELEDD LFDEDLAQLF
EDVSREEGQL NQLFDNKQQH PVINNVSLSE GIVYNQANLT EMQEMRDSCN QVSISTIPTT STAQPETLFN
VTDSQTVEQW LPTEVVPNDV FPTSNYAYIG MQNDSLQAVV SNGQIDYDHS YQSTGQTPLS PLIIGSSGRQ
QQTQTSPGSV TVTATATQSL FDPYHSQRHS FSDCTTDSSS TCSRLSSESP RYTSESSTGT HESRFYGKLA
PSSGSRYQRS SSPRSSQSSI KIARVVPLAS GQRKRGRQSK DEQLASDNEL PVSAFQISEM SLSELQQVLK
NESLSEYQRQ LIRKIRRRGK NKVAARTCRQ RRTDRHDKMS HYI*

FIG. 29

T19E7.2b (spliced)

```
gaATGTCACT TCCATCTGAT TTTGCCTCCT CTCTTCTGGC ATCCTCTACC ACCACCAACA CGACCAAGAC
CGCTCCAGCA GCTGTCAACT CTTTTGACGA ACAAGAAGAA GAATCCAAGA AGATACTGAA CATGTACCTT
CAAATGTTCA ATCAACAACA GGTGGATCAA CACGGCCATC ATCACCAAGA TCCATACGCG TATTCAGGAG
TCTCGAGCAG TTTTGACAGA G[illegible]
[illegible]
[illegible]
[illegible]
TGATTCGTCA TCAACGTGCT CTCGGCTCTG TTCGGAATCT CCACCATACA CGTCAGAGAG CTCAACCGGA
AGTCACGAGT CTCGTTTCTA CGGAAAGTTG GCTCCATCCA GTGGATCACG CTACCAACGA TCATCGTGTC
CACGTTCATC ACAATCTTCG ATTAAGATCG CGAGAGTTGT TCCACTGGCC AGCGGACAAC GCAACGCTGC
ACGTCAATCC AAGGATGAGC AGCTCGCCAG TGACAACGAG CTTCCAGTGT CGGCGTTCCA GATTTCGGAG
ATGTCATTAA GCGAGTTGCA ACAAGTGTTG AAGAACGAGA GTCTCAGCGA GTATCAAAGA CAGTTGATTC
GCAAGATTCG TCGACGCCG[illegible]
[illegible]gaagc cctcttttat cacataaaat ctcggtcgaa accttattaa
agccacataa ttaaagataa ttaattccgc cacaataatc gtttttttct tctttgccgt gtctcatttc
attttgatct actctttcct cccttcggat tctttgattt cccagtgaaa tacctcaccc acttcaatcc
ccacaaagtg agcaacccct atcttgcaac agttttatca tctcttcatc atacccagtt tgataattta
ttatctgatc ccatcccct tgtcgcctct cattagtatc ctagtttttc atttgagccc ggagctcaga
ctacatctcc gaatcatcat acaaatagat agaaacgggt ctcgtgacga aagaatacgt gcaccacacg
acccccccat cctgttcacc cccatacacc tgaaaaatat gatctttaca gttatttcta ttatatcctc
aaatctctcg taatatcgta tcaatttcct cttctttttt gtcattttca atttttctca aatttctcag
atctattctt tttcttgtat ttttggaact tgtatccctc ctccatcccc agacttcccc ttcccagtta
ctcttgtaca ttttcatata tgtccatata tcgtttgaat ctctcattta
```

T19E7.2b (conceptual translation)

```
MSLPSDFASS LLASSTTTNT TNTAPAAVNS FDEQEEESKK ILNMYLQMFN QQQVDQHGHH HQHPYAYSGV
SSTFDRVFPT SNYAYIGMQN DSLQAVVSNG QIDYDHSYQS TGQTPLSPLI IGSSGRQQQT QTSPGSVTVT
ATATQSLFDP YHSQRHSFSD CTTDSSSTCS RLSSESPRYT SESSTGTHES RFYGKLAPSS GSRYQRSSSP
RSSQSSIKIA RVVPLASGQR KRGRQSKDEQ LASDNELPVS AFQISEMSLS ELQQVLKNES LSEYQRQLIR
KIRRRGKNKV AARTCRQRRT DRHDKMSHYI *
```

FIG. 30

T19E7.2a (spliced)

ATGGGCGGTT CATCACGCCG TCAGCGAAGT ACGTCGGCGA CGAGACGAGA CGATAAACGA AGACGAAGAC
AGTGCTTCTC TTCGGTAGCC GACGACGAAG AAGAGACGAC GTCAATTTAT GGAGTGTCG[illegible]
[illegible]
[illegible] ATGTACAGCG
ACAGCAATAA TACGAACTTT GATGAAGTCA ACCATCAGCA TCAACAAGAA CAAGATTTCA ATCGGCAATC
CAAATATGAT TATCCACAAT TCAACCGTCC AATGGGTCTC CGTTGGCGTG ATGATCAACG GATGATGGAG
TATTTCATGT CGAATGGTCC AGTAGAAACT GTTCCAGTTA TGCCAATACT CACCGAGCAT CCACCAGCAT
CTCCATTCGG TAGAGGACCA TCTACAGAAC GTCCAACCAC ATCATCTCGA TACGAGTACA GTTCGCCTTC
TCTCGAGGAT ATCGACTTGA TTGATGTGCT ATGGAGAAGT GATATTGCTG GAGAGAAGGG CACACGACAA
GTGGCTCCTG CTGATCAGTA CGAATGTGAT TTGCAGACGT TGACAGAGAA ATCGACAGTA GCG[illegible]
[illegible]
[illegible] TGACC GAGATGCAAG AGATGCGTGA TTCCTGCAAT
CAAGTTTCGA TTTCAACAAT TCCAACAACA TCGACTGCTC AACCAGAGAC TTTGTTCAAT GTAACCGATT
CACAGACTGT CGAACAGTGG CTTCCAACAG AACTTGTACC AAACGATG[illegible]
[illegible]
[illegible] TGA TTCGTCATCA ACGTGCTCTC GCCTCTCTTC GGAATCTCCA
CGATACACGT CAGAGAGCTC AACCGGAACT CACGAGTCTC GTTTCTACGG AAAGTTGGCT CCATCCAGTG
GATCAGGCTA CCAACGATCA TCGTCTCCAC GTTCATCACA ATCTTCGATT AAGATCGCGA GAGTTGTTCC
ACTGGCCAGC GGACAACGGA AGCGTGGACG TCAATCCAAG GATGAGCAGC TCGCCAGTGA CAACGAGCTT
CCAGTGTCGG CGTTCCAGAT TTCGGAGATG TCATTAAGCG AGTTGCAACA AGTGTTGAAG AACGAGAGTC
TCAGCGAGTA TCAAAGACAG TTGATTCGCA AGATTCGTCG ACGCG[illegible]
[illegible]gaagccct cttttatcac
ataaaatctc ggtcgaaacc ttattaaagc cacataatta aagataatta attccgccac aataatcgtt
tttttcttct ttgccgtgtc tcatttcatt ttgatctact ctttcctccc ttcggattct ttgatttccc
agtgaaatac ctcacccact tcaatcccca caaagtgagc aacccctatc ttgcaacagt tttatcatct
cttcatcata cccagtttga taatttatta tctgatcccc atccccttgt cgcctctcat tagtatccta
gtttttcatt tgagcccgga gctcagacta catctccgaa tcatcataca aatagataga aacgggtctc
gtgacgaaag aatacgtgca ccacacgacc cccccatcct gttcaccccc atacacctga aaaatatgat
ctttacagtt atttctatta tatcctcaaa tctctcgtaa tatcgtatca atttcctctt cttttttgtc
attttcaatt tttctcaaat ttctcagatc tattcttttt cttgtatttt tggaacttgt atccctcctc
catccccaga cttccccttc ccagttactc ttgtacattt tcatatatgt ccatatatcg tttgaatctc
tcatttatgg aaataaattt gaaaaaatc

T19E7.2a (conceptual translation)

MGGSSRRQRS TSATRRDDKR RRRQCFSSVA DDEEETTSIY GVSSIFIWIL ATSSLILVIS SPSSNTSIQS
SSYDRITTKH LLDNISPTFK MYTDSNNRNF DEVNHQHQQE QDFNGQSKYD YPQFNRPMGL RWRDDQRMME
YFMSNGPVET VPVMPILTEH PPASPFGRGP STERPTTSSR YEYSSPSLED IDLIDVLWRS DIAGEKGTRQ
VAPADQYECD LQTLTEKSTV APLTAEENAR YEDLSKGFYN GFFESFNNNQ YQQKHQQQQR EQIKTPTLEH
PTQKAELEDD LFDEDLAQLF EDVSREEGQL NQLFDNKQQH PVINNVSLSE GIVYNQANLT EMQEMRDSCN
QVSISTIPTT STAQPETLFN VTDSQTVEQW LPTEVVPNDV FPTSNYAYIG MQNDSLQAVV SNGQIDYDHS
YQSTGQTPLS PLIIGSSGRQ QQTQTSPGSV TVTATATQSL FDPYHSQRHS FSDCTTDSSS TCSRLSSESP
RYTSESSTGT HESRFYGKLA PSSGSRYQRS SSPRSSQSSI KIARVVPLAS GQRKRGRQSK DEQLASDNEL
PVSAFQISEM SLSELQQVLK NESLSEYQRQ LIRKIRRRGK NKVAARTCRQ RRTDRHDKMS HYI*

FIG. 31

Human Glycogen synthase kinase-3 beta (GSK-3 beta).

```
  1 msgrprttsf aesckpvqqp safgsmkvsr dkdgskvttv vatpgqgpdr pqevsytdtk
 61 vigngsfgvv yqaklcdsge lvaikkvlqd krfknrelqi mrkldhcniv rlryffyssg
121 ekkdevylnl vldyvpetvy rvarhysrak qtlpviyvkl ymyqlfrsla yihsfgichr
181 dikpqnllld pdtavlklcd fgsakqlvrg epnvsyicsr yyrapelifg atdytssidv
241 wsagcvlael llgqpifpgd sgvdqlveii kvlgtptreq iremnpnyte fkfpqikahp
301 wtkvfrprtp peaialcsrl leytptarlt pleacahsff delrdpnvkl pngrdtpalf
361 nfttqelssn pplatilipp hariqaaast ptnataasda ntgdrgqtnn aasasasnst
```

FIG. 32

Human Glycogen synthase kinase-3 alpha (GSK-3 alpha).

```
  1 msgggpsggg pggsgrarts sfaepggggg gggggpggsa sgpggtgggk asvgamgggv
 61 gasssgggpg gsggggsggp gagtsfpppg vklgrdsgkv ttvvatlgqg persqevayt
121 dikvigngsf gvvyqarlae trelvaikkv lqdkrfknre lqimrkldhc nivrlryffy
181 ssgekkdely lnlvleyvpe tvyrvarhft kakltipily vkvymyqlfr slayihsqgv
241 chrdikpqnl lvdpdtavlk lcdfgsakql vrgepnvsyi csryyrapel ifgatdytss
301 idvwsagcvl aelllgqpif pgdsgvdqlv eiikvlgtpt reqiremnpn ytefkfpqik
361 ahpwtkvfks rtppeaialc sslleytpss rlspleacah sffdelrclg tqlpnnrplp
421 plfnfsagel siqpslnail ipphlrspag tttltpssqa ltetptssdw qstdatptlt
481 nss
```

FIG. 33

Mouse Glycogen synthase kinase-3 beta.

```
  1 msgrprttsf aesckpvqqp safgsmkvsr dkdgskvttv vatpgqgpdr pqevsytdtk
 61 vigngsfgvv yqaklcdsge lvaikkvlqd krfknrelqi mrkldhcniv rlryffyssg
121 ekkdevylnl vldyvpetvy rvarhysrak qtlpviyvkl ymyqlfrsla yihsfgichr
181 dikpqnllld pdtavlklcd fgsakqlvrg epnvsyicsr yyrapelifg atdytssidv
241 wsagcvlael llgqpifpgd sgvdqlveii kvlgtptreq iremnpnyte fkfpqikahp
301 wtkvfrprtp peaialcsrl leytptarlt pleacahsff delrdpnvkl pngrdtpalf
361 nfttqelssn pplatilipp hariqaaasp panataasdt nagdrgqtnn aasasasnst
```

FIG. 34

Mouse Glycogen synthase kinase-3 alpha (GSK-3 alpha).

```
  1 masttamdvl eelssdssek qrsvnildsf vkdmferias easflarqar nstinsreiq
 61 tairlllpge lcrrgtgcgk asvwamgggv gasssgvggg sggpgstsfl qpgvklghds
121 rkvttvvatv gqdpersqev actdikvign gsfgvvyqew ladtrelvai kkvlqdkrfk
181 yrelqimckl dhcnivrlqy ffyssgekkd dlylnlvley vpetvyxvar hftkakliip
241 iiyvkvymyq lfrslayihs qgvchrdinl lvdpdtailk lcdfgsakql vlgttvapel
301 ytssidvxsa gcvlaellls qpifpgdngv dqlveiikvl gtptreqire mnpkytefkf
361 pqikahpwtk vfksrtaprp lhsalacwst hhtqgsphlr lvptaslmnc gvsgpapqrp
421 ptspcstsvl vicpsnhlsm pfssllt
```

FIG. 35

GSK-3 [*Caenorhabditis elegans*].

```
  1 mnkqllscsl ksgkqvtmvv asvatdgvdq qveisyydqk vigngsfgvv flaklsttne
 61 mvaikkvlqd krfknrelqi mrklnhpniv klkyffyssg ekkdelylnl ileyvpetvy
121 rvarhyskqr qqipmiyvkl ymyqllrsla yihsigichr dikpqnllid pesgvlklcd
181 fgsakylvrn epnvsyicsr yyrapelifg atnytnsidv wsagtvmael llgqpifpgd
241 sgvdqlveii kvlgtptreq iqsmnpnyke fkfpqikahp wnkvfrvhtp aeaidliski
301 ieytptsrpt pqaacqhaff delrnpdarl psgrplptle mdgpmgtgei sptsgdvagp
361 sa
```

FIG. 36

sgg-1 (GSK-3) inhibits constitutive SKN-1 nuclear accumulation and induction of its target gene _gcs-1_.

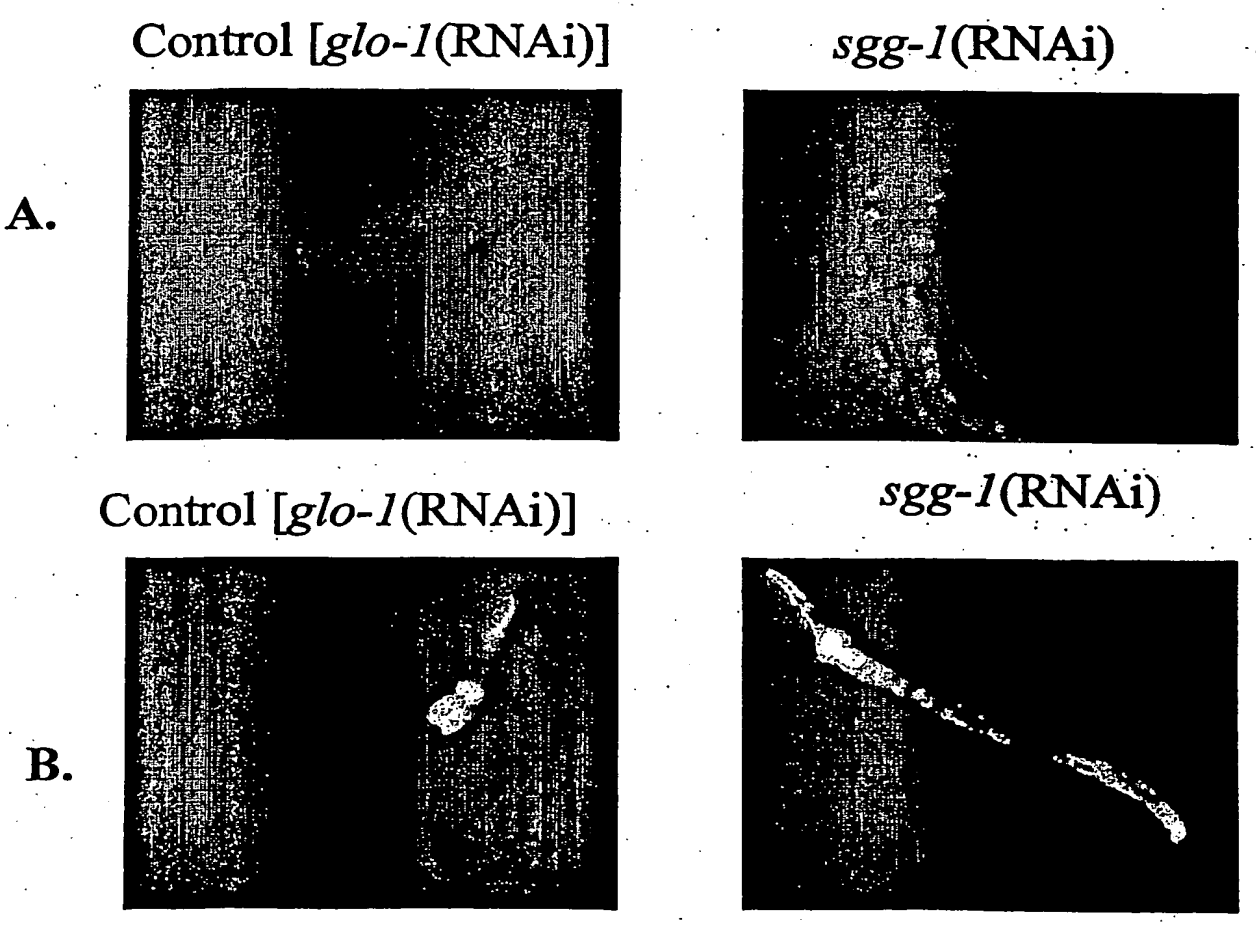
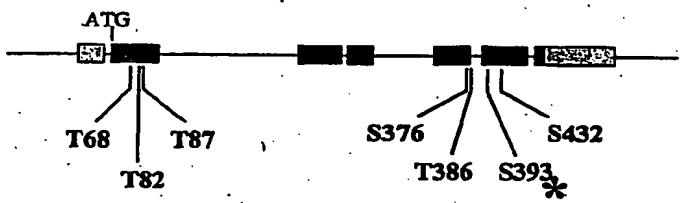


FIG. 37

Ala substitution at a predicted GSK-3 phosphorylation site results in nuclear localization of SKN-1

A.



B.

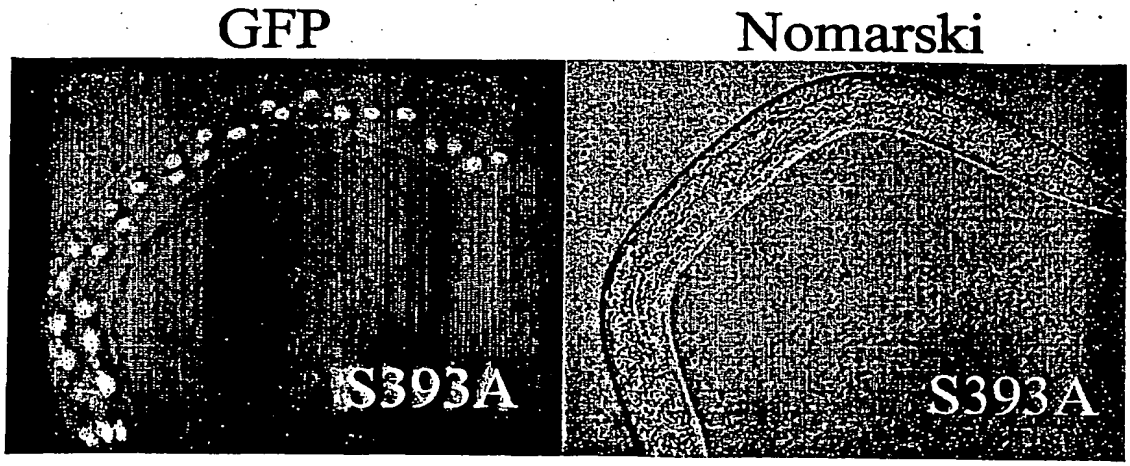
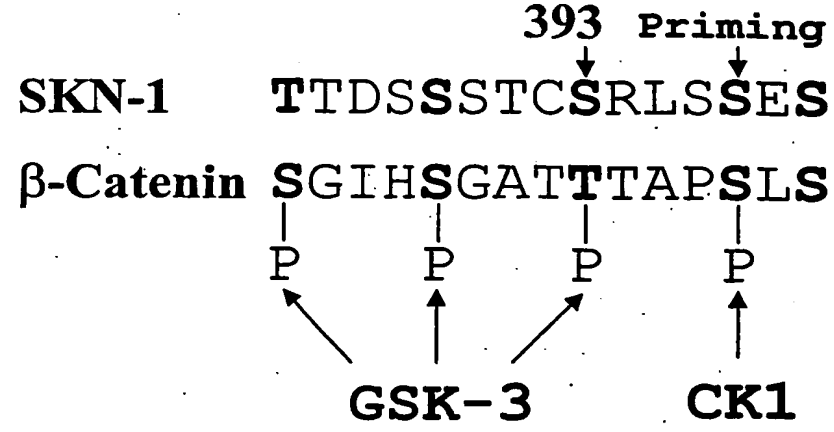


FIG. 38

A.



B.

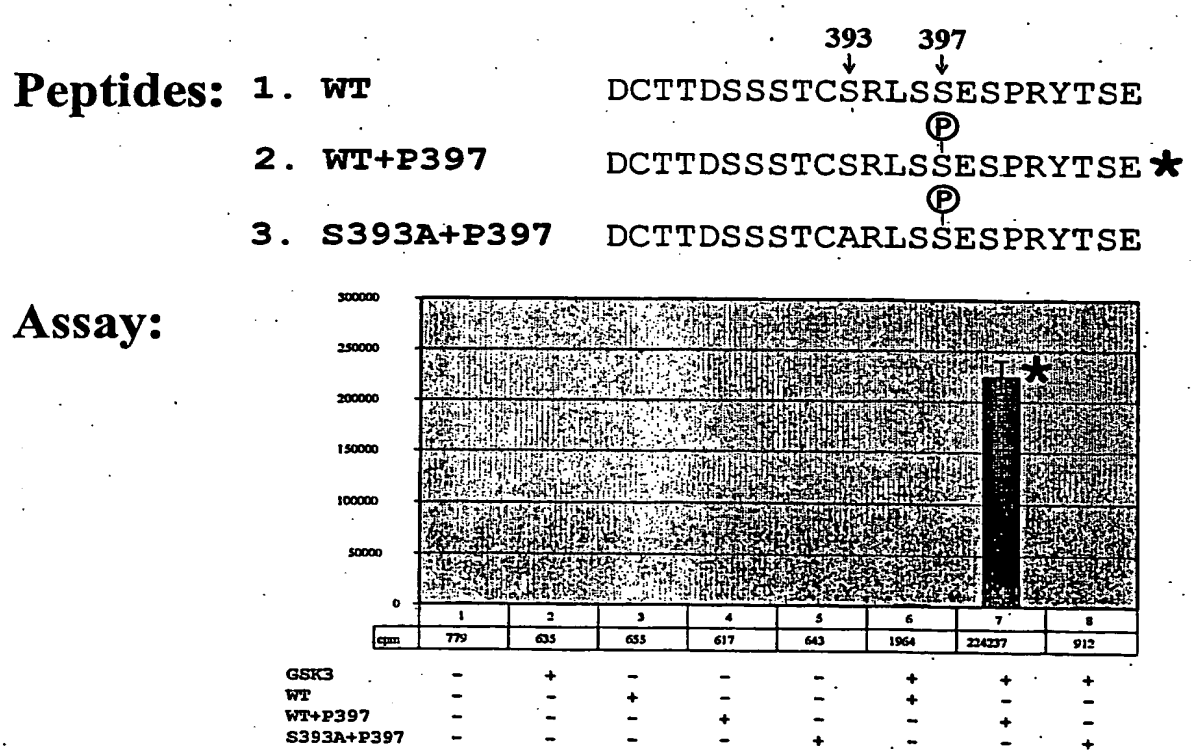


FIG. 39